

SEQUENCE LISTING

<110> Korneluk, Robert G.
Mackenzie, Alexander E.
Baird, Stephen
Liston, Peter

<120> MAMMALIAN IAP GENE FAMILY, PRIMERS,
PROBES, AND DETECTION METHODS

<130> 07891/003005

<150> 08/576,956

<151> 1995-12-22

<150> 08/511,485

<151> 1995-08-04

<160> 92

<170> FastSEQ for Windows Version 4.0

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<212> PRT

<213> artificial sequence based on Homo sapiens, Mus musculus, Cydia pomonella, Orgyia pseudotsugata, and Drosophila melanogaster.

<220>

<221> VARIANT

<222> 8

<223> Glu or Asp

<221> VARIANT

<222> 14,22

<223> Val or Ile

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<222> (1)...(46)

<223> Xaa = Any Amino Acid

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001050-001050

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 <213> artificial sequence based on Homo sapiens, Mus musculus, Cydia pomonella, Orgyia pseudotsugata, and Drosophila melanogaster.

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 <222> 13,16,17
 <223> any amino acid or absent

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26/68

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 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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00654743-090100

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 <213> Homo sapiens

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 35 40 45
 Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val
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 65 70 75 80
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 145 150 155 160
 Ser Tyr Pro Cys Pro Met Asn Asn Glu Asn Ala Arg Leu Leu Thr Phe
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 180 185 190
 Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys
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 Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met Ser Glu
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 245 250 255
 Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu Val Asn
 260 265 270
 Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
 275 280 285
 Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
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 Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
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 Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val Gln Ala
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Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu
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Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys
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Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Leu Gly
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Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser Cys Ser Phe
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			260					265					270		
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		275					280					285			
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Lys	Cys	Phe	Gly	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser	Gly	Asp
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Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu	Phe	Leu
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			340					345					350		
Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Thr	Thr	Gly	Glu
		355					360					365			
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	370					375				380					
Ser	Glu	Asp	Ala	Val	Met	Met	Asn	Thr	Pro	Val	Val	Lys	Ser	Ala	Leu
385					390					395					400
Glu	Met	Gly	Phe	Asn	Arg	Asp	Leu	Val	Lys	Gln	Thr	Val	Leu	Ser	Lys
				405					410					415	
Ile	Leu	Thr	Thr	Gly	Glu	Asn	Tyr	Lys	Thr	Val	Asn	Asp	Ile	Val	Ser
			420					425					430		
Ala	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Glu	Lys	Glu	Lys
			435				440					445			
Gln	Ala	Glu	Glu	Met	Ala	Ser	Asp	Asp	Leu	Ser	Leu	Ile	Arg	Lys	Asn
	450					455					460				
Arg	Met	Ala	Leu	Phe	Gln	Gln	Leu	Thr	Cys	Val	Leu	Pro	Ile	Leu	Asp
465					470					475					480
Asn	Leu	Leu	Lys	Ala	Asn	Val	Ile	Asn	Lys	Gln	Glu	His	Asp	Ile	Ile
				485					490					495	
Lys	Gln	Lys	Thr	Gln	Ile	Pro	Leu	Gln	Ala	Arg	Glu	Leu	Ile	Asp	Thr
			500					505					510		
Ile	Trp	Val	Lys	Gly	Asn	Ala	Ala	Ala	Asn	Ile	Phe	Lys	Asn	Cys	Leu
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Phe	Lys	Asp	Leu	Lys	Lys	Thr	Met	Glu	Glu	Lys	Ile	Gln	Thr	Ser	Gly
385					390					395					400
Ser	Ser	Tyr	Leu	Ser	Leu	Glu	Val	Leu	Ile	Ala	Asp	Leu	Val	Ser	Ala
			405					410						415	
Gln	Lys	Asp	Asn	Thr	Glu	Asp	Glu	Ser	Ser	Gln	Thr	Ser	Leu	Gln	Lys
			420					425					430		
Asp	Ile	Ser	Thr	Glu	Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Lys	Leu
	435						440					445			
Ser	Lys	Ile	Cys	Met	Asp	Arg	Asn	Ile	Ala	Ile	Val	Phe	Phe	Pro	Cys
	450					455					460				
Gly	His	Leu	Ala	Thr	Cys	Lys	Gln	Cys	Ala	Glu	Ala	Val	Asp	Lys	Cys
465					470					475					480
Pro	Met	Cys	Tyr	Thr	Val	Ile	Thr	Phe	Asn	Gln	Lys	Ile	Phe	Met	Ser
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<210> 11
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 <212> PRT
 <213> Orgyia pseudotsugata

Lys	Ala	Ala	Arg	Leu	Gly	Thr	Tyr	Thr	Asn	Trp	Pro	Val	Gln	Phe	Leu
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Glu	Pro	Ser	Arg	Met	Ala	Ala	Ser	Gly	Phe	Tyr	Tyr	Leu	Gly	Arg	Gly
			20					25					30		
Asp	Glu	Val	Arg	Cys	Ala	Phe	Cys	Lys	Val	Glu	Ile	Thr	Asn	Trp	Val
		35					40					45			
Arg	Gly	Asp	Asp	Pro	Glu	Thr	Asp	His	Lys	Arg	Trp	Ala	Pro	Gln	Cys
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Pro	Phe	Val													
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<210> 12
 <211> 275
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 <213> Cydia pomonella

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Trp	Pro	Val	Ser	Phe	Leu	Ser	Pro	Glu	Thr	Met	Ala	Lys	Asn	Gly	Phe
			20					25					30		
Tyr	Tyr	Leu	Gly	Arg	Ser	Asp	Glu	Val	Arg	Cys	Ala	Phe	Cys	Lys	Val
		35					40					45			
Glu	Ile	Met	Arg	Trp	Lys	Glu	Gly	Glu	Asp	Pro	Ala	Ala	Asp	His	Lys
	50					55				60					
Lys	Trp	Ala	Pro	Gln	Cys	Pro	Phe	Val	Lys	Gly	Ile	Asp	Val	Cys	Gly
65				70						75					80
Ser	Ile	Val	Thr	Thr	Asn	Asn	Ile	Gln	Asn	Thr	Thr	Thr	His	Asp	Thr
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<212> PRT
<213> Cydia pomonella
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Ser Pro Glu Thr Met Ala Lys Asn Gly Phe Tyr Tyr Leu Gly Arg Ser
20 25 30
Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Met Arg Trp Lys
35 40 45

Pro Lys Asp Asp Ala Met Ser Glu His Arg Arg His Phe Pro Asn Cys
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 Pro Phe Leu
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<210> 24
 <211> 66
 <212> PRT
 <213> Mus musculus

<400> 24
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 35 40 45
 Ser Glu Asp Pro Trp Asp Gln His Ala Lys Cys Tyr Pro Gly Cys Lys
 50 55 60
 Tyr Leu
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<210> 25
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 25
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 1 5 10 15
 Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
 20 25 30
 Lys Val Lys Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro
 35 40 45
 Ser Glu Asp Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys
 50 55 60
 Tyr Leu
 65

<210> 26
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 26
 His Ala Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu
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 20 25 30
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 35 40 45

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Glu Ser Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg
 50 55 60
 Cys Glu Tyr Leu
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<210> 27
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 27
 His Ala Ala Arg Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro
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 35 40 45
 Glu Ser Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg
 50 55 60
 Cys Glu Phe Leu
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<210> 28
 <211> 68
 <212> PRT
 <213> Orgyia pseudotsugata

<400> 28
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 20 25 30
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 35 40 45
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 50 55 60
 Cys Glu Tyr Val
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<210> 29
 <211> 68
 <212> PRT
 <213> Cydia pomonella

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 35 40 45

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 <212> PRT
 <213> Drosophila melanogaster

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 35 40 45
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 50 55 60
 Cys Gln Phe Val
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 <213> Drosophila melanogaster

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 35 40 45
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 Met Val
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<210> 32
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 32
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 35 40 45

<210> 33
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 33
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 35 40 45

<210> 34
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 34
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 Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
 35 40 45

<210> 35
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 35
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 20 25 30
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 35 40 45

<210> 36
 <211> 46
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 36
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 35 40 45

<210> 37
 <211> 46
 <212> PRT
 <213> *Cydia pomonella*

<400> 37
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 20 25 30
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 35 40 45

<210> 38
 <211> 46
 <212> PRT
 <213> *Orgyia pseudotsugata*

<400> 38
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 <212> DNA
 <213> *Mus musculus*

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 atccccagag aaagacttgt cccttccctt ccctgtcatc tcaccatgaa catggttcaa 180
 gacagcgcct ttctagccaa gctgatgaag agtgctgaca cctttgagtt gaagtatgac 240
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007050" E445960

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cacagaaagt	tgtaccccag	ctgcaacttt	gtacagactt	tgaatccagc	caacagttctg	480
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<212> PRT
<213> Mus musculus
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Leu	Ser	Thr	Tyr	Ser	Ala	Phe	Pro	Arg	Gly	Val	Pro	Val	Ser	Glu	Arg
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Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Ala	Asn	Asp	Lys	Val
	50					55					60				
Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Gln	Gly	Asp
65					70				75						80

Arg	Glu	Ile	Asp	Pro	Ala	Leu	Tyr	Arg	Asp	Ile	Phe	Val	Gln	Gln	Asp
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Ile	Arg	Ser	Leu	Pro	Thr	Asp	Asp	Ile	Ala	Ala	Leu	Pro	Met	Glu	Glu
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Gln	Leu	Arg	Pro	Leu	Pro	Glu	Asp	Arg	Met	Cys	Lys	Val	Cys	Met	Asp
545				550				555				560			
Arg	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val	Cys
565				570				575							
Lys	Asp	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys	Arg	Gly	Thr
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595				600											

<210> 41
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 <212> DNA
 <213> Mus musculus

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Thr	Pro	Gly	Glu	Glu	Asn	Ala	Asp	Pro	Thr	Glu	Thr	Val	Val	His	Phe
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Gly	Pro	Gly	Glu	Ser	Ser	Lys	Asp	Val	Val	Met	Met	Ser	Thr	Pro	Val
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Val	Lys	Ala	Ala	Leu	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Arg	Gln
			370					375					380		
Thr	Val	Gln	Arg	Gln	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Thr	Val
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Asn	Asp	Ile	Val	Ser	Val	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Arg	Arg	Glu
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Leu	Ile	Arg	Lys	Asn	Arg	Met	Ala	Leu	Phe	Gln	Gln	Leu	Thr	His	Val
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Leu	Pro	Ile	Leu	Asp	Asn	Leu	Leu	Glu	Ala	Ser	Val	Ile	Thr	Lys	Gln
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Glu	His	Asp	Ile	Ile	Arg	Gln	Lys	Thr	Gln	Ile	Pro	Leu	Gln	Ala	Arg
					470					475					480
Glu	Leu	Ile	Asp	Thr	Val	Leu	Val	Lys	Gly	Asn	Ala	Ala	Ala	Asn	Ile
				485					490					495	
Phe	Lys	Asn	Ser	Leu	Lys	Gly	Ile	Asp	Ser	Thr	Leu	Tyr	Glu	Asn	Leu
			500					505					510		
Phe	Val	Glu	Lys	Asn	Met	Lys	Tyr	Ile	Pro	Thr	Glu	Asp	Val	Ser	Gly
			515					520					525		
Leu	Ser	Leu	Glu	Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys
			530					535					540		
Lys	Val	Cys	Met	Asp	Arg	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly
					550					555					560
His	Leu	Val	Val	Cys	Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro
				565					570					575	
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<210> 43
 <211> 11
 <212> PRT
 <213> artificial sequence based on Homo sapiens

<400> 43
 Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
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<210> 44
 <211> 635
 <212> PRT
 <213> artificial sequence based on Homo sapiens, Mus musculus, Cydia pomonella, and Drosophila melanogaster

<220>
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 <222> 1,2,3,635
 <223> any amino acid or may be absent

<221> VARIANT
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 <223> Xaa = Any Amino Acid

<400> 44

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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Glu	Xaa	Xaa	Arg	
		20					25				30				
Leu	Xaa	Thr	Phe	Xaa	Xaa	Phe	Pro	Xaa	Xaa	Xaa	Pro	Val	Ser	Xaa	Xaa
		35					40					45			
Xaa	Leu	Ala	Arg	Ala	Gly	Phe	Xaa	Tyr	Thr	Gly	Xaa	Xaa	Asp	Xaa	Val
	50					55					60				
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65					70				75					80	
Ser	Xaa	Xaa	Xaa	Xaa	His	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Cys	Xaa	Phe	Ile
				85					90					95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				100				105						110	
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				115				120						125	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa
				130				135						140	
Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Ser	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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Xaa	Xaa	Xaa	Met	Xaa	Xaa	Glu	Glu	Ala	Arg	Leu	Xaa	Thr	Phe	Xaa	Xaa
			180					185						190	
Trp	Pro	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Pro	Xaa	Glu	Leu	Ala	Xaa	Ala	Gly
	195					200						205			
Phe	Tyr	Tyr	Xaa	Gly	Xaa	Xaa	Asp	Xaa	Val	Xaa	Cys	Phe	Xaa	Cys	Gly
	210				215						220				
Gly	Lys	Leu	Xaa	Asn	Trp	Glu	Pro	Xaa	Asp	Xaa	Ala	Xaa	Ser	Glu	His
225					230					235					240
Xaa	Arg	His	Phe	Pro	Xaa	Cys	Pro	Phe	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				245					250						255
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa
				260				265						270	
Ser	Xaa	Xaa	Xaa	Pro	Xaa	Asn	Pro	Xaa	Met	Ala	Xaa	Xaa	Xaa	Ala	Arg
				275				280						285	
Xaa	Xaa	Thr	Phe	Xaa	Xaa	Trp	Pro	Xaa	Ser	Xaa	Xaa	Val	Xaa	Xaa	Glu
		290				295						300			
Gln	Leu	Ala	Xaa	Ala	Gly	Phe	Tyr	Tyr	Xaa	Gly	Xaa	Gly	Asp	Xaa	Val
305					310					315					320
Lys	Cys	Phe	Xaa	Cys	Xaa	Gly	Gly	Leu	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Asp
				325					330						335
Asp	Pro	Trp	Xaa	Gln	His	Ala	Lys	Trp	Phe	Pro	Xaa	Cys	Xaa	Tyr	Leu
			340					345						350	

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Xaa	Xaa	Xaa	Lys	Gly	Gln	Glu	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
355						360						365					
Xaa	Xaa	Leu	Xaa	Glu	Xaa	Leu	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
370						375						380					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	
385						390						395			400		
Xaa	Xaa	Asp	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Val	Xaa	Xaa	Ala	Xaa	Xaa	
			405						410						415		
Xaa	Met	Gly	Phe	Xaa	Xaa	Xaa	Xaa	Val	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	
			420						425						430		
Ile	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Val	Xaa	Xaa	
435						440						445					
Asp	Leu	Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	
450						455						460					
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465						470						475			480		
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			485						490						495		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
			500						505						510		
Xaa	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	Leu	Gln	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
515						520						525					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
530						535						540					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
545						550						555			560		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Glu	Glu	Xaa	
			565						570						575		
Gln	Leu	Arg	Arg	Leu	Xaa	Glu	Glu	Xaa	Leu	Cys	Lys	Xaa	Cys	Met	Asp	Xaa	
			580						585						590		
Xaa	Glu	Val	Xaa	Xaa	Val	Phe	Xaa	Pro	Cys	Gly	His	Leu	Val	Xaa	Cys	Xaa	
595						600						605					
Xaa	Xaa	Cys	Ala	Xaa	Ser	Val	Xaa	Lys	Cys	Pro	Met	Cys	Arg	Xaa	Xaa	Xaa	
610						615						620					
Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Leu	Ser	Xaa							
625			630						635								

<210> 45
 <211> 204
 <212> DNA
 <213> Homo sapiens

<400> 45
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 aactggcac gagcagggtt tctttataact ggtgaaggag ataccgtgcg gtgcttttagt 120
 tgtcatgcag ctgtagatag atggcaatat ggagactcag cagttggaag acacaggaaa 180
 gtatcccaa attgcagatt tatc 204

<210> 46
 <211> 204
 <212> DNA
 <213> Homo sapiens

<400> 51
 tatgaagcac ggatcggtac ttttggaaaca tggatataact cagttaacaa ggagcagctt 60
 gcaagagctg gatttttatgc ttttaggtgaa ggcgataaag tgaagtgtctt ccactgtgga 120
 ggagggtctca cggattggaa gccaaagtga gacccctggg accagcatgc taagtgtctac 180
 ccagggtgca aataccta 198

<210> 52
 <211> 138
 <212> DNA
 <213> Mus musculus

<400> 52
 gagcagctaa ggcgcctaca agaggagaag ctttcacaaa tctgtatgga tagaaatatt 60
 gctatcggtt tttttccttg tggacatctg gccacttgta aacagtgtgc agaagcagtt 120
 gacaaatgtc ccatgtgc 138

<210> 53
 <211> 204
 <212> DNA
 <213> Homo sapiens

<400> 53
 gaactgtacc gaatgtctac gtattccact tttcctgctg gggttcctgt ctcagaaagg 60
 agtcttgctc gtgctgggtt ctattacact ggtgtgaatg acaagggtcaa atgcttctgt 120
 tgtggcctga tgctggataa ctggaaaaga ggagacagtc ctactgaaaa gcataaaaaag 180
 ttgtatccta gctgcagatt cggt 204

<210> 54
 <211> 201
 <212> DNA
 <213> Homo sapiens

<400> 54
 gaaaatgcc gattacttac ttttcagaca tggccattga cttttctgtc gccaacagat 60
 ctggcacgag caggctttta ctacatagga cctggagaca gagtggcttg ctttgcctgt 120
 ggtggaaaat tgagcaattg ggaaccgaag gataatgcta tgtcagaaca cctgagacat 180
 tttcccaaat gccatttat a 201

<210> 55
 <211> 204
 <212> DNA
 <213> Homo sapiens

<400> 55
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 cagcttgcaa gtgcgggtt ttattatgtg ggtaacagtg atgatgtcaa atgcttttgc 120
 tgtgatggtg gactcaggtg ttgggaatct ggagatgatc catgggttca acatgccaaag 180
 tggtttccaa ggtgtgagta cttg 204

<210> 56
 <211> 138
 <212> DNA
 <213> Homo sapiens

<400> 56
gaacaattgc ggagactacc agaagaaaga acatgtaaag tgtgtatgga caaagaagtg 60
tccatagtgt ttattccttg tggatcatcta gtagtatgca aagattgtgc tccttcttta 120
agaaagtgtc ctatttgt 138

<210> 57
<211> 203
<212> DNA
<213> Mus musculus

<400> 57
agctgtaccg attgtccacg tattcagctt ttcccagggg agttcctgtg tcagaaagga 60
gtctggctcg tgctggcttt tactacactg gtgccaatga caaggtcaag tgcttctgct 120
gtggcctgat gctagacaac tggaaacaag gggacagtcc catggagaag cacagaaagt 180
tgtacccag ctgcaacttt gta 203

<210> 58
<211> 201
<212> DNA
<213> Mus musculus

<400> 58
gagaaggcca gattactcac ctatgaaaca tggccattgt cttttctgtc accagcaaag 60
ctggccaaag caggcttcta ctacatagga cctggagata gaggggcctg ctttgcgtgc 120
gatgggaaac tgagcaactg ggaacgtaag gatgatgcta tgtcagagca ccagaggcat 180
ttcccagct gtccgttctt a 201

<210> 59
<211> 204
<212> DNA
<213> Mus musculus

<400> 59
cacgcagccc gtattagaac attctctaac tggccttcta gtgcactagt tcattcccag 60
gaacttgcaa gtgcgggctt ttattataca ggacacagtg atgatgtcaa gtgtttatgc 120
tgtgatgggtg ggctgagggtg ctgggaatct ggagatgacc cctgggtgga acatgccaa 180
tggtttccaa ggtgtgagta cttg 204

<210> 60
<211> 138
<212> DNA
<213> Mus musculus

<400> 60
gaacagttgc ggcccctccc ggaggacaga atgtgtaaag tgtgtatgga ccgagaggta 60
tccatcgtgt tcattccctg tggccatctg gtcgtgtgca aagactgcgc tccctctctg 120
aggaagtgtc ccatctgt 138

<210> 61
<211> 204
<212> DNA
<213> Homo sapiens

<400> 66
gaagaggcca gatttctttac ttacagtatg tggccttttaa gttttctgtc accagcagag 60
ctggccagag ctggcttcta ttacataggg cctggagaca gggaggcctg ttttgcctgt 120
ggtaggaaac tgagcaactg ggaaccaaag gattatgcta tgtagagca ccgcagacat 180
tttcccact gtccatttct g 201

<210> 67
<211> 204
<212> DNA
<213> Mus musculus

<400> 67
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cagcttgcaa gtgctggatt ctattacgtg gatcgcaatg atgatgtcaa gtgcctttgt 120
tgtgatgggtg gcttgagatg ttgggaacct ggagatgacc cctggataga acacgccaaa 180
tggtttccaa ggtgtgagtt cttg 204

<210> 68
<211> 114
<212> DNA
<213> Mus musculus

<400> 68
gaacgaactt gcaaagtgtg tatggacaga gaggtttcta ttgtgttcat tccgtgtggt 60
catctagtag tctgccagga atgtgcccct tctctaagga agtgcccat ctgc 114

<210> 69
<211> 68
<212> PRT
<213> Homo sapiens

<400> 69
Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Gly Ser Pro
1 5 10 15
Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
20 25 30
Gly Asp Thr Val Arg Cys Phe Ser Cys His Ala Ala Val Asp Arg Trp
35 40 45
Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Lys Val Ser Pro Asn
50 55 60
Cys Arg Phe Ile
65

<210> 70
<211> 68
<212> PRT
<213> Homo sapiens

<400> 70
Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
1 5 10 15
Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ile
20 25 30

Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
 35 40 45
 Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60
 Cys Phe Phe Val
 65

<210> 71
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 71
 Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
 1 5 10 15
 Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
 20 25 30
 Lys Val Lys Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro
 35 40 45
 Ser Glu Asp Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys
 50 55 60
 Tyr Leu
 65

<210> 72
 <211> 46
 <212> PRT
 213> Homo sapiens

<400> 72
 Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Cys Lys Ile Cys Met
 1 5 10 15
 Asp Arg Asn Ile Ala Ile Val Phe Val Pro Cys Gly His Leu Val Thr
 20 25 30
 Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
 35 40 45

<210> 73
 <211> 68
 <212> PRT
 <213> Mus musculus

<400> 73
 Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Ser Ser Pro
 1 5 10 15
 Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
 20 25 30
 Gly Asp Thr Val Gln Cys Phe Ser Cys His Ala Ala Ile Asp Arg Trp
 35 40 45

Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Arg Ile Ser Pro Asn
 50 55 60
 Cys Arg Phe Ile
 65

<210> 74
 <211> 68
 <212> PRT
 <213> Mus musculus

<400> 74
 Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
 1 5 10 15
 Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ala
 20 25 30
 Asp Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
 35 40 45
 Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60
 Cys Phe Phe Val
 65

<210> 75
 <211> 66
 <212> PRT
 <213> Mus musculus

<400> 75
 Tyr Glu Ala Arg Ile Val Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
 1 5 10 15
 Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
 20 25 30
 Lys Val Lys Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro
 35 40 45
 Ser Glu Asp Pro Trp Asp Gln His Ala Lys Cys Tyr Pro Gly Cys Lys
 50 55 60
 Tyr Leu
 65

<210> 76
 <211> 46
 <212> PRT
 <213> Mus musculus

<400> 76
 Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Ser Lys Ile Cys Met
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 Asp Arg Asn Ile Ala Ile Val Phe Phe Pro Cys Gly His Leu Ala Thr
 20 25 30
 Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
 35 40 45

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<210> 77
 <211> 68
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 <213> Homo sapiens

<400> 77
 Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
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 Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
 20 25 30
 Asn Asp Lys Val Lys Cys Phe Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45
 Lys Arg Gly Asp Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser
 50 55 60
 Cys Arg Phe Val
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<210> 78
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 78
 Glu Asn Ala Arg Leu Leu Thr Phe Gln Thr Trp Pro Leu Thr Phe Leu
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 Ser Pro Thr Asp Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
 Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
 35 40 45
 Pro Lys Asp Asn Ala Met Ser Glu His Leu Arg His Phe Pro Lys Cys
 50 55 60
 Pro Phe Ile
 65

<210> 79
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 79
 His Ala Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu
 1 5 10 15
 Val Asn Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn
 20 25 30
 Ser Asp Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp
 35 40 45
 Glu Ser Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg
 50 55 60
 Cys Glu Tyr Leu
 65

<210> 80
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 80
 Glu Gln Leu Arg Arg Leu Pro Glu Glu Arg Thr Cys Lys Val Cys Met
 1 5 10 15
 Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val
 20 25 30
 Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
 35 40 45

<210> 81
 <211> 68
 <212> PRT
 <213> Mus musculus

<400> 81
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 1 5 10 15
 Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Ala
 20 25 30
 Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45
 Lys Gln Gly Asp Ser Pro Met Glu Lys His Arg Lys Leu Tyr Pro Ser
 50 55 60
 Cys Asn Phe Val
 65

<210> 82
 <211> 67
 <212> PRT
 <213> Mus musculus

<400> 82
 Glu Lys Ala Arg Leu Leu Thr Tyr Glu Thr Trp Pro Leu Ser Phe Leu
 1 5 10 15
 Ser Pro Ala Lys Leu Ala Lys Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
 Asp Arg Val Ala Cys Phe Ala Cys Asp Gly Lys Leu Ser Asn Trp Glu
 35 40 45
 Arg Lys Asp Asp Ala Met Ser Glu His Gln Arg His Phe Pro Ser Cys
 50 55 60
 Pro Phe Leu
 65

<210> 83
 <211> 68
 <212> PRT
 <213> Mus musculus

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<400> 83

His Ala Ala Arg Ile Arg Thr Phe Ser Asn Trp Pro Ser Ser Ala Leu
 1 5 10 15
 Val His Ser Gln Glu Leu Ala Ser Ala Gly Phe Tyr Tyr Thr Gly His
 20 25 30
 Ser Asp Asp Val Lys Cys Leu Cys Cys Asp Gly Gly Leu Arg Cys Trp
 35 40 45
 Glu Ser Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg
 50 55 60
 Cys Glu Tyr Leu
 65

<210> 84

<211> 46

<212> PRT

<213> Mus musculus

<400> 84

Glu Gln Leu Arg Pro Leu Pro Glu Asp Arg Met Cys Lys Val Cys Met
 1 5 10 15
 Asp Arg Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val
 20 25 30
 Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
 35 40 45

<210> 85

<211> 68

<212> PRT

<213> Homo sapiens

<400> 85

Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
 1 5 10 15
 Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
 20 25 30
 Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45
 Lys Leu Gly Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser
 50 55 60
 Cys Ser Phe Ile
 65

<210> 86

<211> 67

<212> PRT

<213> Homo sapiens

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<211> 68
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<210> 88
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<210> 89
<211> 68
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<400> 89

Glu Leu Tyr Arg Met Ser Thr Tyr Ser Ala Phe Pro Arg Gly Val Pro
1 5 10 15
Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
20 25 30

Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
35 40 45
Lys Gln Gly Asp Ser Pro Val Glu Lys His Arg Gln Phe Tyr Pro Ser
50 55 60
Cys Ser Phe Val
65

<210> 90

<211> 67

<212> PRT

<213> Mus musculus

<400> 90

Glu Glu Ala Arg Phe Leu Thr Tyr Ser Met Trp Pro Leu Ser Phe Leu
1 5 10 15
Ser Pro Ala Glu Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
20 25 30
Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
35 40 45
Pro Lys Asp Tyr Ala Met Ser Glu His Arg Arg His Phe Pro His Cys
50 55 60
Pro Phe Leu
65

<210> 91

<211> 68

<212> PRT

<213> Mus musculus

<400> 91

His Ser Ala Arg Leu Arg Thr Phe Leu Tyr Trp Pro Pro Ser Val Pro
1 5 10 15
Val Gln Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Asp Arg
20 25 30
Asn Asp Asp Val Lys Cys Leu Cys Cys Asp Gly Gly Leu Arg Cys Trp
35 40 45
Glu Pro Gly Asp Asp Pro Trp Ile Glu His Ala Lys Trp Phe Pro Arg
50 55 60
Cys Glu Phe Leu
65

<210> 92

<211> 38

<212> PRT

<213> Mus musculus

<400> 92

Glu Arg Thr Cys Lys Val Cys Met Asp Arg Glu Val Ser Ile Val Phe

1

5

10

15

Ile Pro Cys Gly His Leu Val Val Cys Gln Glu Cys Ala Pro Ser Leu

20

25

30

Arg Lys Cys Pro Ile Cys

35

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Korneluk, Robert G.
Mackenzie, Alexander E.
Baird, Stephen
- (ii) TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
PROBES, AND DETECTION METHODS
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fish & Richardson P.C.
(B) STREET: 225 Franklin Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/511,485
(B) FILING DATE: 04-AUG-1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Clark, Paul T.
(B) REGISTRATION NUMBER: 30,162
(C) REFERENCE/DOCKET NUMBER: 07891/002001
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617/542-5070
(B) TELEFAX: 617/542-8906
(C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
(D) OTHER INFORMATION: Xaa at positons 2, 3, 4, 5,

096574-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAAAGGTGG	ACAAAGTCCTA	TTTTCAAGAG	AAGATGACTT	TTAACAGTTT	TGAAGGATCT	60
AAAACTTGTG	TACCTGCAGA	CATCAATAAG	GAAGAAGAAT	TTGTAGAAGA	GTTTAATAGA	120
TTAAAACTT	TTGCTAATTT	TCCAAGTGGT	AGTCCTGTTT	CAGCATCAAC	ACTGGCACGA	180
GCAGGGTTTC	TTTATACTGG	TGAAGGAGAT	ACCGTGCGGT	GCTTTAGTTG	TCATGCAGCT	240
GTAGATAGAT	GGCAATATGG	AGACTCAGCA	GTTGGAAGAC	ACAGGAAAGT	ATCCCCAAAT	300
TGCAGATTTA	TCAACGGCTT	TTATCTTGAA	AATAGTGCCA	CGCAGTCTAC	AAATTCTGGT	360
ATCCAGAATG	GTCAGTACAA	AGTTGAAAAC	TATCTGGGAA	GCAGAGATCA	TTTTGCCTTA	420
GACAGGCCAT	CTGAGACACA	TGCAGACTAT	CTTTTGAGAA	CTGGGCAGGT	TGTAGATATA	480
TCAGACACCA	TATACCCGAG	GAACCCTGCC	ATGTATTGTG	AAGAAGCTAG	ATTAAAGTCC	540
TTTCAGAACT	GGCCAGACTA	TGCTCACCTA	ACCCCAAGAG	AGTTAGCAAG	TGCTGGACTC	600
TACTACACAG	GTATTGGTGA	CCAAGTGCAG	TGCTTTTGTT	GTGGTGGAAA	ACTGAAAAAT	660
TGGGAACCTT	GTGATCGTGC	CTGGTCAGAA	CACAGGCGAC	ACTTTCCTAA	TTGCTTCTTT	720
GTTTTGGGCC	GGAATCTTAA	TATTCGAAGT	GAATCTGATG	CTGTGAGTTC	TGATAGGAAT	780
TTCCCAAATT	CAACAAATCT	TCCAAGAAAT	CCATCCATGG	CAGATTATGA	AGCACGGATC	840
TTTACTTTTG	GGACATGGAT	ATACTCAGTT	AACAAGGAGC	AGCTTGCAAG	AGCTGGATTT	900
TATGCTTTAG	GTGAAGGTGA	TAAAGTAAAG	TGCTTTCACT	GTGGAGGAGG	GCTAACTGAT	960
TGGAAGCCCA	GTGAAGACCC	TTGGGAACAA	CATGCTAAAT	GGTATCCAGG	GTGCAAATAT	1020
CTGTTAGAAC	AGAAGGGACA	AGAATATATA	AACAATATTC	ATTAACTCA	TTCACTTGAG	1080
GAGTGTCTGG	TAAGAACTAC	TGAGAAAACA	CCATCACTAA	CTAGAAGAAT	TGATGATACC	1140
ATCTTCCAAA	ATCCTATGGT	ACAAGAAGCT	ATACGAATGG	GGTTCAGTTT	CAAGGACATT	1200
AAGAAAATAA	TGGAGGAAAA	AATTCAGATA	TCTGGGAGCA	ACTATAAATC	ACTTGAGGTT	1260
CTGGTTGCAG	ATCTAGTGAA	TGCTCAGAAA	GACAGTATGC	AAGATGAGTC	AAGTCAGACT	1320
TCATTACAGA	AAGAGATTAG	TACTGAAGAG	CAGCTAAGGC	GCCTGCAAGA	GGAGAAGCTT	1380
TGCAAAATCT	GTATGGATAG	AAATATTGCT	ATCGTTTTTG	TTCCTTGTGG	ACATCTAGTC	1440
ACTTGTAAC	AATGTGCTGA	AGCAGTTGAC	AAGTGTCCCA	TGTGCTACAC	AGTCATTACT	1500
TTCAAGCAAA	AAATTTTTAT	GTCTTAATCT	AACTCTATAG	TAGGCATGTT	ATGTTGTTCT	1560
TATTACCCTG	ATTGAATGTG	TGATGTGAAC	TGACTTTAAG	TAATCAGGAT	TGAATTCCAT	1620
TAGCATTTGC	TACCAAGTAG	GAAAAAAAT	GTACATGGCA	GTGTTTTAGT	TGGCAATATA	1680
ATCTTTGAAT	TTCTTGATTT	TTCAGGGTAT	TAGCTGTATT	ATCCATTTTT	TTTACTGTTA	1740

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TTTAATTGAA ACCATAGACT AAGAATAAGA AGCATCATAC TATAACTGAA CACAATGTGT 1800
 ATTCATAGTA TACTGATTTA ATTTCTAAGT GTAAGTGAAT TAATCATCTG GATTTTTTTAT 1860
 TCTTTTCAGA TAGGCTTAAC AAATGGAGCT TTCTGTATAT AAATGTGGAG ATTAGAGTTA 1920
 ATCTCCCCAA TCACATAATT TGTTTTGTGT GAAAAAGGAA TAAATTGTTT CATGCTGGTG 1980
 GAAAGATAGA GATTGTTTTT AGAGGTTGGT TGTTGTGTTT TAGGATTCTG TCCATTTTCT 2040
 TGTAAGGGA TAAACACGGA CGTGTGCGAA ATATGTTTGT AAAGTGATTT GCCATTGTTG 2100
 AAAGCGTATT TAATGATAGA ATACTATCGA GCCAACATGT ACTGACATGG AAAGATGTCA 2160
 GAGATATGTT AAGTGTAATA TGCAAGTGGC GGGACACTAT GTATAGTCTG AGCCAGATCA 2220
 AAGTATGTAT GTTGTTAATA TGCATAGAAC GAGAGATTTG GAAAGATATA CACCAAACCTG 2280
 TTAAATGTGG TTTCTCTTCG GGGAGGGGGG GATTGGGGGA GGGGCCCCAG AGGGGTTTTA 2340
 GAGGGGCCTT TTCACTTTCG ACTTTTTTCA TTTTGTTCTG TTCGGATTTT TTATAAGTAT 2400
 GTAGACCCCG AAGGGTTTTA TGGGAACATA CATCAGTAAC CTAACCCCG TGACTATCCT 2460
 GTGCTCTTCC TAGGGAGCTG TGTTGTTTCC CACCCACCAC CCTTCCCTCT GAACAAATGC 2520
 CTGAGTGCTG GGGCACTTTN 2540

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 497 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Phe Asn Ser Phe Glu Gly Ser Lys Thr Cys Val Pro Ala Asp
 1 5 10 15
 Ile Asn Lys Glu Glu Glu Phe Val Glu Glu Phe Asn Arg Leu Lys Thr
 20 25 30
 Phe Ala Asn Phe Pro Ser Gly Ser Pro Val Ser Ala Ser Thr Leu Ala
 35 40 45
 Arg Ala Gly Phe Leu Tyr Thr Gly Glu Gly Asp Thr Val Arg Cys Phe
 50 55 60
 Ser Cys His Ala Ala Val Asp Arg Trp Gln Tyr Gly Asp Ser Ala Val
 65 70 75 80
 Gly Arg His Arg Lys Val Ser Pro Asn Cys Arg Phe Ile Asn Gly Phe
 85 90 95
 Tyr Leu Glu Asn Ser Ala Thr Gln Ser Thr Asn Ser Gly Ile Gln Asn

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100										105										110																																		
Gly	Gln	Tyr	Lys	Val	Glu	Asn	Tyr	Leu	Gly	Ser	Arg	Asp	His	Phe	Ala																																							
		115					120					125																																										
Leu	Asp	Arg	Pro	Ser	Glu	Thr	His	Ala	Asp	Tyr	Leu	Leu	Arg	Thr	Gly																																							
		130					135					140																																										
Gln	Val	Val	Asp	Ile	Ser	Asp	Thr	Ile	Tyr	Pro	Arg	Asn	Pro	Ala	Met																																							
		145				150				155					160																																							
Tyr	Cys	Glu	Glu	Ala	Arg	Leu	Lys	Ser	Phe	Gln	Asn	Trp	Pro	Asp	Tyr																																							
				165					170					175																																								
Ala	His	Leu	Thr	Pro	Arg	Glu	Leu	Ala	Ser	Ala	Gly	Leu	Tyr	Tyr	Thr																																							
				180				185					190																																									
Gly	Ile	Gly	Asp	Gln	Val	Gln	Cys	Phe	Cys	Cys	Gly	Gly	Lys	Leu	Lys																																							
		195					200					205																																										
Asn	Trp	Glu	Pro	Cys	Asp	Arg	Ala	Trp	Ser	Glu	His	Arg	Arg	His	Phe																																							
		210				215					220																																											
Pro	Asn	Cys	Phe	Phe	Val	Leu	Gly	Arg	Asn	Leu	Asn	Ile	Arg	Ser	Glu																																							
		225			230					235					240																																							
Ser	Asp	Ala	Val	Ser	Ser	Asp	Arg	Asn	Phe	Pro	Asn	Ser	Thr	Asn	Leu																																							
				245					250					255																																								
Pro	Arg	Asn	Pro	Ser	Met	Ala	Asp	Tyr	Glu	Ala	Arg	Ile	Phe	Thr	Phe																																							
				260				265					270																																									
Gly	Thr	Trp	Ile	Tyr	Ser	Val	Asn	Lys	Glu	Gln	Leu	Ala	Arg	Ala	Gly																																							
		275					280					285																																										
Phe	Tyr	Ala	Leu	Gly	Glu	Gly	Asp	Lys	Val	Lys	Cys	Phe	His	Cys	Gly																																							
		290				295				300																																												
Gly	Gly	Leu	Thr	Asp	Trp	Lys	Pro	Ser	Glu	Asp	Pro	Trp	Glu	Gln	His																																							
		305				310				315				320																																								
Ala	Lys	Trp	Tyr	Pro	Gly	Cys	Lys	Tyr	Leu	Leu	Glu	Gln	Lys	Gly	Gln																																							
				325					330					335																																								
Glu	Tyr	Ile	Asn	Asn	Ile	His	Leu	Thr	His	Ser	Leu	Glu	Glu	Cys	Leu																																							
				340				345					350																																									
Val	Arg	Thr	Thr	Glu	Lys	Thr	Pro	Ser	Leu	Thr	Arg	Arg	Ile	Asp	Asp																																							
				355			360					365																																										
Thr	Ile	Phe	Gln	Asn	Pro	Met	Val	Gln	Glu	Ala	Ile	Arg	Met	Gly	Phe																																							
						375				380																																												
Ser	Phe	Lys	Asp	Ile	Lys	Lys	Ile	Met	Glu	Glu	Lys	Ile	Gln	Ile	Ser																																							
					390				395					400																																								
Gly	Ser	Asn	Tyr	Lys	Ser	Leu	Glu	Val	Leu	Val	Ala	Asp	Leu	Val	Asn																																							
				405				410					415																																									
Ala	Gln	Lys	Asp	Ser	Met	Gln	Asp	Glu	Ser	Ser	Gln	Thr	Ser	Leu	Gln																																							
			420					425					430																																									

Lys Glu Ile Ser Thr Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys
 435 440 445

Leu Cys Lys Ile Cys Met Asp Arg Asn Ile Ala Ile Val Phe Val Pro
 450 455 460

Cys Gly His Leu Val Thr Cys Lys Gln Cys Ala Glu Ala Val Asp Lys
 465 470 475 480

Cys Pro Met Cys Tyr Thr Val Ile Thr Phe Lys Gln Lys Ile Phe Met
 485 490 495

Ser

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCTTGAGAT GTATCAGTAT AGGATTTAGG ATCTCCATGT TGGAAGTCTA AATGCATAGA	60
AATGGAAATA ATGGAAATTT TTCATTTTGG CTTTTCAGCC TAGTATTAAA ACTGATAAAA	120
GCAAAGCCAT GCACAAAACT ACCTCCCTAG AGAAAGGCTA GTCCCTTTTC TTCCCCATTC	180
ATTTTCATTAT GAACATAGTA GAAAACAGCA TATTCTTATC AAATTTGATG AAAAGCGCCA	240
ACACGTTTGA ACTGAAATAC GACTTGTCAT GTGAAGTCTA CCGAATGTCT ACGTATTCCA	300
CTTTTCCTGC TGGGGTTTCT GTCTCAGAAA GGAGTCTTGC TCGTGCTGGT TTCTATTACA	360
CTGGTGTGAA TGACAAGGTC AAATGCTTCT GTTGTGGCCT GATGCTGGAT AACTGGAAAA	420
GAGGAGACAG TCCTACTGAA AAGCATAAAA AGTTGTATCC TAGCTGCAGA TTCGTTTCTA	480
GTCTAAATTC CGTTAACAAC TTGGAAGCTA CCTCTCAGCC TACTTTTCTT TCTTCAGTAA	540
CACATTCCAC AACTCATTG CTTCCGGGTA CAGAAAACAG TGGATATTTT CGTGGCTCTT	600
ATTCAAACTC TCCATCAAAT CCTGTAAACT CCAGAGCAAA TCAAGAATTT TCTGCCTTGA	660
TGAGAAGTTC CTACCCCTGT CCAATGAATA ACGAAAATGC CAGATTACTT ACTTTTCAGA	720
CATGGCCATT GACTTTTCTG TCGCCAACAG ATCTGGCAGC AGCAGGCTTT TACTACATAG	780
GACCTGGAGA CAGAGTGGCT TGCTTTGCCT GTGGTGAAAA ATTGAGCAAT TGGGAACCGA	840
AGGATAATGC TATGTCAGAA CACCTGAGAC ATTTTCCCAA ATGCCCATTT ATAGAAAATC	900
AGCTTCAAGA CACTTCAAGA TACACAGTTT CTAATCTGAG CATGCAGACA CATGCAGCCC	960

GCTTTAAAAC ATTCTTTAAC TGGCCCTCTA GTGTTCTAGT TAATCCTGAG CAGCTTGCAA	1020
GTGCGGGTTT TTATTATGTG GGTAACAGTG ATGATGTCAA ATGCTTTTGC TGTGATGGTG	1080
GACTCAGGTG TTGGGAATCT GGAGATGATC CATGGGTTCA ACATGCCAAG TGGTTTCCAA	1140
GGTGTGAGTA CTTGATAAGA ATTAAAGGAC AGGAGTTCAT CCGTCAAGTT CAAGCCAGTT	1200
ACCCTCATCT ACTTGAACAG CTGCTATCCA CATCAGACAG CCCAGGAGAT GAAAATGCAG	1260
AGTCATCAAT TATCCATTTG GAACCTGGAG AAGACCATTG AGAAGATGCA ATCATGATGA	1320
ATACTCCTGT GATTAATGCT GCCGTGGAAA TGGGCTTTAG TAGAAGCCTG GTAAAACAGA	1380
CAGTTCAGAG AAAAATCCTA GCAACTGGAG AGAATTATAG ACTAGTCAAT GATCTTGTGT	1440
TAGACTTACT CAATGCAGAA GATGAAATAA GGGAAGAGGA GAGAGAAAGA GCAACTGAGG	1500
AAAAAGAATC AAATGATTTA TTATTAATCC GGAAGAATAG AATGGCACTT TTTCAACATT	1560
TGACTTGTGT AATTCCAATC CTGGATAGTC TACTAACTGC CGGAATTATT AATGAACAAG	1620
AACATGATGT TATTAAACAG AAGACACAGA CGTCTTTACA AGCAAGAGAA CTGATTGATA	1680
CGATTTTAGT AAAAGGAAAT ATTGCAGCCA CTGTATTCAG AAACCTCTCTG CAAGAAGCTG	1740
AAGCTGTGTT ATATGAGCAT TTATTTGTGC AACAGGACAT AAAATATATT CCCACAGAAG	1800
ATGTTTCAGA TCTACCAAGT GAAGAACAAT TGCAGGAGACT ACCAGAAGAA AGAACATGTA	1860
AAGTGTGTAT GGACAAAGAA GTGTCCATAG TGTTTATTCC TTGTGGTCAT CTAGTAGTAT	1920
GCAAAGATTG TGCTCCTTCT TTAAGAAAGT GTCCTATTTG TAGGAGTACA ATCAAGGGTA	1980
CAGTTCGTAC ATTTCTTTCA TGAAGAAGAA CAAAACATC GTCTAAACTT TAGAATTAAT	2040
TTATTAAATG TATTATAACT TTAACCTTTA TCCTAATTTG GTTTCCTTAA AATTTTTATT	2100
TATTTACAAC TCAAAAAACA TTGTTTTGTG TAACATATTT ATATATGTAT CTAAACCATA	2160
TGAACATATA TTTTTTAGAA ACTAAGAGAA TGATAGGCTT TTGTTCTTAT GAACGAAAAA	2220
GAGGTAGCAC TACAAACACA ATATTCAATC CAAATTCAG CATTATTGAA ATTGTAAGTG	2280
AAGTAAAACT TAAGATATTT GAGTTAACCT TTAAGAATTT TAAATATTTT GGCATTGTAC	2340
TAATACCGGG AACATGAAGC CAGGTGTGGT GGTATGTACC TGTAGTCCCA GGCTGAGGCA	2400
AGAGAATTAC TTGAGCCCAG GAGTTTGAAT CCATCCTGGG CAGCATACTG AGACCCTGCC	2460
TTTAAAAACN AACAGNACCA AANCCAAACA CCAGGGACAC ATTTCTCTGT CTTTTTTGAT	2520
CAGTGTCCTA TACATCGAAG GTGTGCATAT ATGTTGAATC ACATTTTAGG GACATGGTGT	2580
TTTATAAAG AATTCTGTGA GNAAAAATTT AATAAAGCAA CCAAATTACT CTTAAAAAAA	2640
AAAAAAAAAA AAAAAAATCG AGGGGCCCCG ACCAAT	2676

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 604 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asn	Ile	Val	Glu	Asn	Ser	Ile	Phe	Leu	Ser	Asn	Leu	Met	Lys	Ser	1	5	10	15
Ala	Asn	Thr	Phe	Glu	Leu	Lys	Tyr	Asp	Leu	Ser	Cys	Glu	Leu	Tyr	Arg	20	25	30	
Met	Ser	Thr	Tyr	Ser	Thr	Phe	Pro	Ala	Gly	Val	Pro	Val	Ser	Glu	Arg	35	40	45	
Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Val	Asn	Asp	Lys	Val	50	55	60	
Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Arg	Gly	Asp	65	70	75	80
Ser	Pro	Thr	Glu	Lys	His	Lys	Lys	Leu	Tyr	Pro	Ser	Cys	Arg	Phe	Val	85	90	95	
Gln	Ser	Leu	Asn	Ser	Val	Asn	Asn	Leu	Glu	Ala	Thr	Ser	Gln	Pro	Thr	100	105	110	
Phe	Pro	Ser	Ser	Val	Thr	His	Ser	Thr	His	Ser	Leu	Leu	Pro	Gly	Thr	115	120	125	
Glu	Asn	Ser	Gly	Tyr	Phe	Arg	Gly	Ser	Tyr	Ser	Asn	Ser	Pro	Ser	Asn	130	135	140	
Pro	Val	Asn	Ser	Arg	Ala	Asn	Gln	Glu	Phe	Ser	Ala	Leu	Met	Arg	Ser	145	150	155	160
Ser	Tyr	Pro	Cys	Pro	Met	Asn	Asn	Glu	Asn	Ala	Arg	Leu	Leu	Thr	Phe	165	170	175	
Gln	Thr	Trp	Pro	Leu	Thr	Phe	Leu	Ser	Pro	Thr	Asp	Leu	Ala	Arg	Ala	180	185	190	
Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys	195	200	205	
Gly	Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asn	Ala	Met	Ser	Glu	210	215	220	
His	Leu	Arg	His	Phe	Pro	Lys	Cys	Pro	Phe	Ile	Glu	Asn	Gln	Leu	Gln	225	230	235	240
Asp	Thr	Ser	Arg	Tyr	Thr	Val	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala	245	250	255	
Ala	Arg	Phe	Lys	Thr	Phe	Phe	Asn	Trp	Pro	Ser	Ser	Val	Leu	Val	Asn	260	265	270	

Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
275 280 285

Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
290 295 300

Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
305 310 315 320

Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val Gln Ala
325 330 335

Ser Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Ser Pro
340 345 350

Gly Asp Glu Asn Ala Glu Ser Ser Ile Ile His Leu Glu Pro Gly Glu
355 360 365

Asp His Ser Glu Asp Ala Ile Met Met Asn Thr Pro Val Ile Asn Ala
370 375 380

Ala Val Glu Met Gly Phe Ser Arg Ser Leu Val Lys Gln Thr Val Gln
385 390 395 400

Arg Lys Ile Leu Ala Thr Gly Glu Asn Tyr Arg Leu Val Asn Asp Leu
405 410 415

Val Leu Asp Leu Leu Asn Ala Glu Asp Glu Ile Arg Glu Glu Glu Arg
420 425 430

Glu Arg Ala Thr Glu Glu Lys Glu Ser Asn Asp Leu Leu Leu Ile Arg
435 440 445

Lys Asn Arg Met Ala Leu Phe Gln His Leu Thr Cys Val Ile Pro Ile
450 455 460

Leu Asp Ser Leu Leu Thr Ala Gly Ile Ile Asn Glu Gln Glu His Asp
465 470 475 480

Val Ile Lys Gln Lys Thr Gln Thr Ser Leu Gln Ala Arg Glu Leu Ile
485 490 495

Asp Thr Ile Leu Val Lys Gly Asn Ile Ala Ala Thr Val Phe Arg Asn
500 505 510

Ser Leu Gln Glu Ala Glu Ala Val Leu Tyr Glu His Leu Phe Val Gln
515 520 525

Gln Asp Ile Lys Tyr Ile Pro Thr Glu Asp Val Ser Asp Leu Pro Val
530 535 540

Glu Glu Gln Leu Arg Arg Leu Pro Glu Glu Arg Thr Cys Lys Val Cys
545 550 555 560

Met Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val
565 570 575

Val Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg
580 585 590

Ser Thr Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
595 600

00554743-090100

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTAGGTTACC TGAAAGAGTT ACTACAACCC CAAAGAGTTG TGTTCTAAGT AGTATCTTGG 60
TAATTCAGAG AGATACTCAT CCTACCTGAA TATAAACTGA GATAAATCCA GTAAAGAAAG 120
TGTAGTAAAT TCTACATAAG AGTCTATCAT TGATTTCTTT TTGTGGTGGA AATCTTAGTT 180
CATGTGAAGA AATTTTCATGT GAATGTTTTA GCTATCAAAC AGTACTGTCA CCTACTCATG 240
CACAAAACCTG CCTCCCAAAG ACTTTTCCCA GGTCCCTCGT ATCAAAACAT TAAGAGTATA 300
ATGGAAGATA GCACGATCTT GTCAGATTGG ACAAACAGCA ACAAACAAAA AATGAAGTAT 360
GACTTTTCCT GTGAACTCTA CAGAATGTCT ACATATTCAA CTTTCCCCGC CGGGGTGCCT 420
GTCTCAGAAA GGAGTCTTGC TCGTGCTGGT TTTTATTATA CTGGTGTGAA TGACAAGGTC 480
AAATGCTTCT GTTGTGGCCT GATGCTGGAT AACTGGAAAC TAGGAGACAG TCCTATTCAA 540
AAGCATAAAC AGCTATATCC TAGCTGTAGC TTTATTGAGA ATCTGGTTTC AGCTAGTCTG 600
GGATCCACCT CTAAGAATAC GTCTCCAATG AGAAACAGTT TTGCACATTC ATTATCTCCC 660
ACCTTGGAAC ATAGTAGCTT GTTCAGTGGT TCTTACTCCA GCCTTCCTCC AAACCCTCTT 720
AATTCTAGAG CAGTTGAAGA CATCTCTTCA TCGAGGACTA ACCCCTACAG TTATGCAATG 780
AGTACTGAAG AAGCCAGATT TCTTACCTAC CATATGTGGC CATTAACTTT TTTGTCACCA 840
TCAGAATTGG CAAGAGCTGG TTTTATTAT ATAGGACCTG GAGATAGGGT AGCCTGCTTT 900
GCCTGTGGTG GGAAGCTCAG TAACTGGGAA CCAAGGATG ATGCTATGTC AGAACACCGG 960
AGGCATTTTC CCAACTGTCC ATTTTGGAA AATTCTCTAG AAACCTGAG GTTTAGCATT 1020
TCAAATCTGA GCATGCAGAC ACATGCAGCT CGAATGAGAA CATTATATGTA CTGGCCATCT 1080
AGTGTTCCAG TTCAGCCTGA GCAGCTTGCA AGTGCTGGTT TTTATTATGT GGGTCGCAAT 1140
GATGATGTCA AATGCTTTGG TTGTGATGGT GGCTTGAGGT GTTGGGAATC TGGAGATGAT 1200
CCATGGGTAG AACATGCCAA GTGGTTTCCA AGGTGTGAGT TCTTGATACG AATGAAAGGC 1260
CAAGAGTTTG TTGATGAGAT TCAAGGTAGA TATCCTCATC TTCTTGAACA GCTGTTGTCA 1320
ACTTCAGATA CCACTGGAGA AGAAAATGCT GACCCACCAA TTATTCATTT TGGACCTGGA 1380
GAAAGTTCTT CAGAAGATGC TGTCATGATG AATACACCTG TGGTTAAATC TGCCTTGGA 1440

ATGGGCTTTA ATAGAGACCT GGTGAAACAA ACAGTTCTAA GTAAATCCT GACAACTGGA 1500
GAGAACTATA AAACAGTTAA TGATATTGTG TCAGCACTTC TTAATGCTGA AGATGAAAAA 1560
AGAGAAGAGG AGAAGGAAAA ACAAGCTGAA GAAATGGCAT CAGATGATTT GTCATTAATT 1620
CGGAAGAACA GAATGGCTCT CTTTCAACAA TTGACATGTG TGCTTCCTAT CCTGGATAAT 1680
CTTTTAAAGG CCAATGTAAT TAATAAACAG GAACATGATA TTATTAAACA AAAAACACAG 1740
ATACCTTTAC AAGCGAGAGA ACTGATTGAT ACCATTTGGG TTAAAGGAAA TGCTGCGGCC 1800
AACATCTTCA AAAACTGTCT AAAAGAAATT GACTCTACAT TGTATAAGAA CTTATTTGTG 1860
GATAAGAATA TGAAGTATAT TCCAACAGAA GATGTTTCAG GTCTGTCACT GGAAGAACAA 1920
TTGAGGAGGT TGCAAGAAGA ACGAACTTGT AAAGTGTGTA TGGACAAAGA AGTTTCTGTT 1980
GTATTTATTC CTTGTGGTCA TCTGGTAGTA TGCCAGGAAT GTGCCCCCTC TCTAAGAAAA 2040
TGCCCTATTT GCAGGGGTAT AATCAAGGGT ACTGTTTCGTA CATTTCTCTC TTAAAGAAAA 2100
ATAGTCTATA TTTTAACCTG CATAAAAAGG TCTTTAAAT ATTGTTGAAC ACTTGAAGCC 2160
ATCTAAAGTA AAAAGGGAAT TATGAGTTTT TCAATTAGTA ACATTCATGT TCTAGTCTGC 2220
TTTGGTACTA ATAATCTTGT TTCTGAAAAG ATGGTATCAT ATATTTAATC TTAATCTGTT 2280
TATTTACAAG GGAAGATTTA TGTTTGGTGA ACTATATTAG TATGTATGTG TACCTAAGGG 2340
AGTAGCGTCN CTGCTTGTTA TGCATCATTT CAGGAGTTAC TGGATTTGTT GTTCTTTCAG 2400
AAAGCTTTGA ANACTAAATT ATAGTGTAGA AAAGAAGCTG AAACCAGGAA CTCTGGAGTT 2460
CATCAGAGTT ATGGTGCCGA ATTGTCTTTG GTGCTTTTCA CTTGTGTTTT AAAATAAGGA 2520
TTTTTCTCTT ATTTCTCCCC CTAGTTTGTG AGAAACATCT CAATAAAGTG CTTTAAAAAG 2580

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 618 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met His Lys Thr Ala Ser Gln Arg Leu Phe Pro Gly Pro Ser Tyr Gln
1 5 10 15
Asn Ile Lys Ser Ile Met Glu Asp Ser Thr Ile Leu Ser Asp Trp Thr
20 25 30
Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr
35 40 45

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Arg	Met	Ser	Thr	Tyr	Ser	Thr	Phe	Pro	Ala	Gly	Val	Pro	Val	Ser	Glu	50	55	60
Arg	Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Val	Asn	Asp	Lys	65	70	75
Val	Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Leu	Gly	85	90	95
Asp	Ser	Pro	Ile	Gln	Lys	His	Lys	Gln	Leu	Tyr	Pro	Ser	Cys	Ser	Phe	100	105	110
Ile	Gln	Asn	Leu	Val	Ser	Ala	Ser	Leu	Gly	Ser	Thr	Ser	Lys	Asn	Thr	115	120	125
Ser	Pro	Met	Arg	Asn	Ser	Phe	Ala	His	Ser	Leu	Ser	Pro	Thr	Leu	Glu	130	135	140
His	Ser	Ser	Leu	Phe	Ser	Gly	Ser	Tyr	Ser	Ser	Leu	Pro	Pro	Asn	Pro	145	150	155
Leu	Asn	Ser	Arg	Ala	Val	Glu	Asp	Ile	Ser	Ser	Ser	Arg	Thr	Asn	Pro	165	170	175
Tyr	Ser	Tyr	Ala	Met	Ser	Thr	Glu	Glu	Ala	Arg	Phe	Leu	Thr	Tyr	His	180	185	190
Met	Trp	Pro	Leu	Thr	Phe	Leu	Ser	Pro	Ser	Glu	Leu	Ala	Arg	Ala	Gly	195	200	205
Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys	Gly	210	215	220
Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asp	Ala	Met	Ser	Glu	His	225	230	235
Arg	Arg	His	Phe	Pro	Asn	Cys	Pro	Phe	Leu	Glu	Asn	Ser	Leu	Glu	Thr	245	250	255
Leu	Arg	Phe	Ser	Ile	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala	Ala	Arg	260	265	270
Met	Arg	Thr	Phe	Met	Tyr	Trp	Pro	Ser	Ser	Val	Pro	Val	Gln	Pro	Glu	275	280	285
Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Arg	Asn	Asp	Asp	Val	290	295	300
Lys	Cys	Phe	Gly	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser	Gly	Asp	305	310	315
Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu	Phe	Leu	325	330	335
Ile	Arg	Met	Lys	Gly	Gln	Glu	Phe	Val	Asp	Glu	Ile	Gln	Gly	Arg	Tyr	340	345	350
Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Thr	Thr	Gly	Glu	355	360	365
Glu	Asn	Ala	Asp	Pro	Pro	Ile	Ile	His	Phe	Gly	Pro	Gly	Glu	Ser	Ser	370	375	380

Ser Glu Asp Ala Val Met Met Asn Thr Pro Val Val Lys Ser Ala Leu
385 390 395 400

Glu Met Gly Phe Asn Arg Asp Leu Val Lys Gln Thr Val Leu Ser Lys
405 410 415

Ile Leu Thr Thr Gly Glu Asn Tyr Lys Thr Val Asn Asp Ile Val Ser
420 425 430

Ala Leu Leu Asn Ala Glu Asp Glu Lys Arg Glu Glu Glu Lys Glu Lys
435 440 445

Gln Ala Glu Glu Met Ala Ser Asp Asp Leu Ser Leu Ile Arg Lys Asn
450 455 460

Arg Met Ala Leu Phe Gln Gln Leu Thr Cys Val Leu Pro Ile Leu Asp
465 470 475 480

Asn Leu Leu Lys Ala Asn Val Ile Asn Lys Gln Glu His Asp Ile Ile
485 490 495

Lys Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr
500 505 510

Ile Trp Val Lys Gly Asn Ala Ala Ala Asn Ile Phe Lys Asn Cys Leu
515 520 525

Lys Glu Ile Asp Ser Thr Leu Tyr Lys Asn Leu Phe Val Asp Lys Asn
530 535 540

Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly Leu Ser Leu Glu Glu
545 550 555 560

Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met Asp
565 570 575

Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val Cys
580 585 590

Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg Gly Ile
595 600 605

Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
610 615

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACACTCTGC TGGGCGGCGG GCCGCCCTCC TCCGGGACCT CCCCTCGGGA ACCGTCGCCC

60

GCGGCGCTTA	GTTAGGACTG	GAGTGCTTGG	CGCGAAAAGG	TGGACAAGTC	CTATTTTCCA	120
GAGAAGATGA	CTTTTAACAG	TTTTGAAGGA	ACTAGAACTT	TTGTACTTGC	AGACACCAAT	180
AAGGATGAAG	AATTTGTAGA	AGAGTTTAAT	AGATTAAAAA	CATTTGCTAA	CTTCCCAAGT	240
AGTAGTCCTG	TTTCAGCATC	AACATTGGCG	CGAGCTGGGT	TTCTTTATAC	CGGTGAAGGA	300
GACACCGTGC	AATGTTTCAG	TTGTCATGCG	GCAATAGATA	GATGGCAGTA	TGGAGACTCA	360
GCTGTTGGAA	GACACAGGAG	AATATCCCCA	AATTGCAGAT	TTATCAATGG	TTTTTATTTT	420
GAAAATGGTG	CTGCACAGTC	TACAAATCCT	GGTATCCAAA	ATGGCCAGTA	CAAATCTGAA	480
AACTGTGTGG	GAAATAGAAA	TCCTTTTGCC	CCTGACAGGC	CACCTGAGAC	TCATGCTGAT	540
TATCTCTTGA	GAAGTGGACA	GGTTGTAGAT	ATTTTCAGACA	CCATATACCC	GAGGAACCCCT	600
GCCATGTGTA	GTGAAGAAGC	CAGATTGAAG	TCATTTCAGA	ACTGGCCGGA	CTATGCTCAT	660
TTAACCCCCA	GAGAGTTAGC	TAGTGCTGGC	CTCTACTACA	CAGGGGCTGA	TGATCAAGTG	720
CAATGCTTTT	GTTGTGGGGG	AAAAGTAAA	AATTGGGAAC	CCTGTGATCG	TGCCTGGTCA	780
GAACACAGGA	GACACTTTCC	CAATTGCTTT	TTTGTTTTGG	GCCGGAACGT	TAATGTTCTGA	840
AGTGAATCTG	GTGTGAGTTC	TGATAGGAAT	TTCCCAAATT	CAACAAACTC	TCCAAGAAAT	900
CCAGCCATGG	CAGAATATGA	AGCACGGATC	GTTACTTTTG	GAACATGGAT	ATACTCAGTT	960
AACAAGGAGC	AGCTTGCAAG	AGCTGGATTT	TATGCTTTAG	GTGAAGGCCA	TAAAGTGAAG	1020
TGCTTCCACT	GTGGAGGAGG	GCTCACGGAT	TGGAAGCCAA	GTGAAGACCC	CTGGGACCAG	1080
CATGCTAAGT	GCTACCCAGG	GTGCAAATAC	CTATTGGATG	AGAAGGGGCA	AGAATATATA	1140
AATAATATTC	ATTTAACCCA	TCCACTTGAG	GAATCTTTGG	GAAGAACTGC	TGAAAAAACA	1200
CCACCGCTAA	CTAAAAAAAT	CGATGATACC	ATCTTCCAGA	ATCCTATGGT	GCAAGAAGCT	1260
ATACGAATGG	GATTTAGCTT	CAAGGACCTT	AAGAAAACAA	TGGAAGAAAA	AATCCAAACA	1320
TCCGGGAGCA	GCTATCTATC	ACTTGAGGTC	CTGATTGCAG	ATCTTGTGAG	TGCTCAGAAA	1380
GATAATACGG	AGGATGAGTC	AAGTCAAAC	TCATTGCAGA	AAGACATTAG	TACTGAAGAG	1440
CAGCTAAGGC	GCCTACAAGA	GGAGAAGCTT	TCCAAAATCT	GTATGGATAG	AAATATTGCT	1500
ATCGTTTTTT	TTCCTTGTGG	ACATCTGGCC	ACTTGTAAC	AGTGTGCAGA	AGCAGTTGAC	1560
AAATGTCCCA	TGTGCTACAC	CGTCATTACG	TTCAACCAAA	AAATTTTAT	GTCTTAGTGG	1620
GGCACCACAT	GTTATGTTCT	TCTTGCTCTA	ATTGAATGTG	TAATGGGAGC	GAACTTTAAG	1680
TAATCCTGCA	TTTGCAATCC	ATTAGCATCC	TGCTGTTTCC	AAATGGAGAC	CAATGCTAAC	1740
AGCACTGTTT	CCGTCTAAAC	ATTCAATTC	TGGATCTTTC	GAGTTATCAG	CTGTATCATT	1800
TAGCCAGTGT	TTTACTCGAT	TGAAACCTTA	GACAGAGAAG	CATTTTATAG	CTTTTCACAT	1860
GTATATTGGT	AGTACACTGA	CTTGATTCT	ATATGTAAGT	GAATTCATCA	CCTGCATGTT	1920

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210	215	220
Pro Asn Cys Phe Phe Val Leu Gly Arg Asn Val Asn Val Arg Ser Glu		
225	230	235
Ser Gly Val Ser Ser Asp Arg Asn Phe Pro Asn Ser Thr Asn Ser Pro		
	245	250
Arg Asn Pro Ala Met Ala Glu Tyr Glu Ala Arg Ile Val Thr Phe Gly		
	260	265
Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu Ala Arg Ala Gly Phe		
	275	280
Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys Cys Phe His Cys Gly Gly		
	290	295
Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro Trp Asp Gln His Ala		
	305	310
Lys Cys Tyr Pro Gly Cys Lys Tyr Leu Leu Asp Glu Lys Gly Gln Glu		
	325	330
Tyr Ile Asn Asn Ile His Leu Thr His Pro Leu Glu Glu Ser Leu Gly		
	340	345
Arg Thr Ala Glu Lys Thr Pro Pro Leu Thr Lys Lys Ile Asp Asp Thr		
	355	360
Ile Phe Gln Asn Pro Met Val Gln Glu Ala Ile Arg Met Gly Phe Ser		
	370	375
Phe Lys Asp Leu Lys Lys Thr Met Glu Glu Lys Ile Gln Thr Ser Gly		
	385	390
Ser Ser Tyr Leu Ser Leu Glu Val Leu Ile Ala Asp Leu Val Ser Ala		
	405	410
Gln Lys Asp Asn Thr Glu Asp Glu Ser Ser Gln Thr Ser Leu Gln Lys		
	420	425
Asp Ile Ser Thr Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu		
	435	440
Ser Lys Ile Cys Met Asp Arg Asn Ile Ala Ile Val Phe Phe Pro Cys		
	450	455
Gly His Leu Ala Thr Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys		
	465	470
Pro Met Cys Tyr Thr Val Ile Thr Phe Asn Gln Lys Ile Phe Met Ser		
	485	490
		495

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Ala Ala Arg Leu Gly Thr Tyr Thr Asn Trp Pro Val Gln Phe Leu
1 5 10 15
Glu Pro Ser Arg Met Ala Ala Ser Gly Phe Tyr Tyr Leu Gly Arg Gly
20 25 30
Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Thr Asn Trp Val
35 40 45
Arg Gly Asp Asp Pro Glu Thr Asp His Lys Arg Trp Ala Pro Gln Cys
50 55 60
Pro Phe Val
65

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Asp Leu Arg Leu Glu Glu Val Arg Leu Asn Thr Phe Glu Lys
1 5 10 15
Trp Pro Val Ser Phe Leu Ser Pro Glu Thr Met Ala Lys Asn Gly Phe
20 25 30
Tyr Tyr Leu Gly Arg Ser Asp Glu Val Arg Cys Ala Phe Cys Lys Val
35 40 45
Glu Ile Met Arg Trp Lys Glu Gly Glu Asp Pro Ala Ala Asp His Lys
50 55 60
Lys Trp Ala Pro Gln Cys Pro Phe Val Lys Gly Ile Asp Val Cys Gly
65 70 75 80
Ser Ile Val Thr Thr Asn Asn Ile Gln Asn Thr Thr Thr His Asp Thr
85 90 95
Ile Ile Gly Pro Ala His Pro Lys Tyr Ala His Glu Ala Ala Arg Val
100 105 110
Lys Ser Phe His Asn Trp Pro Arg Cys Met Lys Gln Arg Pro Glu Gln
115 120 125
Met Ala Asp Ala Gly Phe Phe Tyr Thr Gly Tyr Gly Asp Asn Thr Lys

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130	135	140
Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp Glu Pro Glu Asp Val		
145	150	155 160
<hr/>		
Pro Trp Glu Gln His Val Arg Trp Phe Asp Arg Cys Ala Tyr Val Gln		
	165	170 175
Leu Val Lys Gly Arg Asp Tyr Val Gln Lys Val Ile Thr Glu Ala Cys		
	180	185 190
Val Leu Pro Gly Glu Asn Thr Thr Val Ser Thr Ala Ala Pro Val Ser		
	195	200 205
Glu Pro Ile Pro Glu Thr Lys Ile Glu Lys Glu Pro Gln Val Glu Asp		
	210	215 220
Ser Lys Leu Cys Lys Ile Cys Tyr Val Glu Glu Cys Ile Val Cys Phe		
	225	230 235 240
Val Pro Cys Gly His Val Val Ala Cys Ala Lys Cys Ala Leu Ser Val		
	245	250 255
Asp Lys Cys Pro Met Cys Arg Lys Ile Val Thr Ser Val Leu Lys Val		
	260	265 270
Tyr Phe Ser		
	275	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Thr Glu Leu Gly Met Glu Leu Glu Ser Val Arg Leu Ala Thr Phe	
1	5 10 15
Gly Glu Trp Pro Leu Asn Ala Pro Val Ser Ala Glu Asp Leu Val Ala	
	20 25 30
Asn Gly Phe Phe Ala Thr Gly Lys Trp Leu Glu Ala Glu Cys His Phe	
	35 40 45
Cys His Val Arg Ile Asp Arg Trp Glu Tyr Gly Asp Gln Val Ala Glu	
	50 55 60
Arg His Arg Arg Ser Ser Pro Ile Cys Ser Met Val Leu Ala Pro Asn	
	65 70 75 80
His Cys Gly Asn Val Pro Arg Ser Gln Glu Ser Asp Asn Glu Gly Asn	
	85 90 95

Ser Val Val Asp Ser Pro Glu Ser Cys Ser Cys Pro Asp Leu Leu Leu
100 105 110

Glu Ala Asn Arg Leu Val Thr Phe Lys Asp Trp Pro Asn Pro Asn Ile
115 120 125

Thr Pro Gln Ala Leu Ala Lys Ala Gly Phe Tyr Tyr Leu Asn Arg Leu
130 135 140

Asp His Val Lys Cys Val Trp Cys Asn Gly Val Ile Ala Lys Trp Glu
145 150 155 160

Lys Asn Asp Asn Ala Phe Glu Glu His Lys Arg Phe Phe Pro Gln Cys
165 170 175

Pro Arg Val Gln Met Gly Pro Leu Ile Glu Phe Ala Thr Gly Lys Asn
180 185 190

Leu Asp Glu Leu Gly Ile Gln Pro Thr Thr Leu Pro Leu Arg Pro Lys
195 200 205

Tyr Ala Cys Val Asp Ala Arg Leu Arg Thr Phe Thr Asp Trp Pro Ile
210 215 220

Ser Asn Ile Gln Pro Ala Ser Ala Leu Ala Gln Ala Gly Leu Tyr Tyr
225 230 235 240

Gln Lys Ile Gly Asp Gln Val Arg Cys Phe His Cys Asn Ile Gly Leu
245 250 255

Arg Ser Trp Gln Lys Glu Asp Glu Pro Trp Phe Glu His Ala Lys Trp
260 265 270

Ser Pro Lys Cys Gln Phe Val Leu Leu Ala Lys Gly Pro Ala Tyr Val
275 280 285

Ser Glu Val Leu Ala Thr Thr Ala Ala Asn Ala Ser Ser Gln Pro Ala
290 295 300

Thr Ala Pro Ala Pro Thr Leu Gln Ala Asp Val Leu Met Asp Glu Ala
305 310 315 320

Pro Ala Lys Glu Ala Leu Thr Leu Gly Ile Asp Gly Gly Val Val Arg
325 330 335

Asn Ala Ile Gln Arg Lys Leu Leu Ser Ser Gly Cys Ala Phe Ser Thr
340 345 350

Leu Asp Glu Leu Leu His Asp Ile Phe Asp Asp Ala Gly Ala Gly Ala
355 360 365

Ala Leu Glu Val Arg Glu Pro Pro Glu Pro Ser Ala Pro Phe Ile Glu
370 375 380

Pro Cys Gln Ala Thr Thr Ser Lys Ala Ala Ser Val Pro Ile Pro Val
385 390 395 400

Ala Asp Ser Ile Pro Ala Lys Pro Gln Ala Ala Glu Ala Val Ser Asn
405 410 415

Ile Ser Lys Ile Thr Asp Glu Ile Gln Lys Met Ser Val Ser Thr Pro
420 425 430

Asn Gly Asn Leu Ser Leu Glu Glu Glu Asn Arg Gln Leu Lys Asp Ala
 435 440 445

Arg Leu Cys Lys Val Cys Leu Asp Glu Glu Val Gly Val Val Phe Leu
 450 455 460

Pro Cys Gly His Leu Ala Thr Cys Asn Gln Cys Ala Pro Ser Val Ala
 465 470 475 480

Asn Cys Pro Met Cys Arg Ala Asp Ile Lys Gly Phe Val Arg Thr Phe
 485 490 495

Leu Ser

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Glu Val Arg Leu Asn Thr Phe Glu Lys Trp Pro Val Ser Phe Leu
 1 5 10 15
 Ser Pro Glu Thr Met Ala Lys Asn Gly Phe Tyr Tyr Leu Gly Arg Ser
 20 25 30
 Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Met Arg Trp Lys
 35 40 45
 Glu Gly Glu Asp Pro Ala Ala Asp His Lys Lys Trp Ala Pro Gln Cys
 50 55 60
 Pro Phe Val
 65

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Ala Asn Arg Leu Val Thr Phe Lys Asp Trp Pro Asn Pro Asn Ile
 1 5 10 15

Thr Pro Gln Ala Leu Ala Lys Ala Gly Phe Tyr Tyr Leu Asn Arg Leu
 20 25 30

Asp His Val Lys Cys Val Trp Cys Asn Gly Val Ile Ala Lys Trp Glu
 35 40 45

Lys Asn Asp Asn Ala Phe Glu Glu His Lys Arg Phe Phe Pro Gln Cys
 50 55 60

Pro Arg Val
 65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Ser Ser Pro
 1 5 10 15

Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
 20 25 30

Gly Asp Thr Val Gln Cys Phe Ser Cys His Ala Ala Ile Asp Arg Trp
 35 40 45

Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Arg Ile Ser Pro Asn
 50 55 60

Cys Arg Phe Ile
 65

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Gly Ser Pro
 1 5 10 15

Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
 20 25 30

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Gly Asp Thr Val Arg Cys Phe Ser Cys His Ala Ala Val Asp Arg Trp
 35 40 45
 Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Lys Val Ser Pro Asn
 50 55 60
 Cys Arg Phe Ile
 65

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
 1 5 10 15
 Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
 20 25 30
 Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45
 Lys Arg Gly Asp Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser
 50 55 60
 Cys Arg Phe Val
 65

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
 1 5 10 15
 Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
 20 25 30
 Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45

Lys Leu Gly Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser
 50 55 60
 Cys Ser Phe Ile
 65

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
 1 5 10 15
 Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ala
 20 25 30
 Asp Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
 35 40 45
 Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60
 Cys Phe Phe Val
 65

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
 1 5 10 15
 Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ile
 20 25 30
 Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
 35 40 45
 Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60

Cys Phe Phe Val
65

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Asn Ala Arg Leu Leu Thr Phe Gln Thr Trp Pro Leu Thr Phe Leu
1 5 10 15
Ser Pro Thr Asp Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
 35 40 45
Pro Lys Asp Asn Ala Met Ser Glu His Leu Arg His Phe Pro Lys Cys
50 55 60
Pro Phe Ile
65

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Glu Ala Arg Phe Leu Thr Tyr His Met Trp Pro Leu Thr Phe Leu
1 5 10 15
Ser Pro Ser Glu Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
 35 40 45
Pro Lys Asp Asp Ala Met Ser Glu His Arg Arg His Phe Pro Asn Cys
50 55 60
Pro Phe Leu
65

SECRET

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

[illegible]

75

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

His Ala Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu
1           5           10           15
Val Asn Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn
20           25           30
Ser Asp Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp
35           40           45
Glu Ser Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg
50           55           60
Cys Glu Tyr Leu
65
  
```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

His Ala Ala Arg Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro
1           5           10           15
Val Gln Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg
20           25           30
Asn Asp Asp Val Lys Cys Phe Gly Cys Asp Gly Gly Leu Arg Cys Trp
35           40           45
Glu Ser Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg
50           55           60
Cys Glu Phe Leu
65
  
```

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Glu	Ala	Ala	Arg	Leu	Arg	Thr	Phe	Ala	Glu	Trp	Pro	Arg	Gly	Leu	Lys
1				5					10					15	
Gln	Arg	Pro	Glu	Glu	Leu	Ala	Glu	Ala	Gly	Phe	Phe	Tyr	Thr	Gly	Gln
			20					25					30		
Gly	Asp	Lys	Thr	Arg	Cys	Phe	Cys	Cys	Asp	Gly	Gly	Leu	Lys	Asp	Trp
		35					40					45			
Glu	Pro	Asp	Asp	Ala	Pro	Trp	Gln	Gln	His	Ala	Arg	Trp	Tyr	Asp	Arg
		50				55					60				
Cys	Glu	Tyr	Val												
			65												

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Glu	Ala	Ala	Arg	Val	Lys	Ser	Phe	His	Asn	Trp	Pro	Arg	Cys	Met	Lys
1				5					10					15	
Gln	Arg	Pro	Glu	Gln	Met	Ala	Asp	Ala	Gly	Phe	Phe	Tyr	Thr	Gly	Tyr
			20					25					30		
Gly	Asp	Asn	Thr	Lys	Cys	Phe	Tyr	Cys	Asp	Gly	Gly	Leu	Lys	Asp	Trp
		35					40					45			
Glu	Pro	Glu	Asp	Val	Pro	Trp	Glu	Gln	His	Val	Arg	Trp	Phe	Asp	Arg
		50				55					60				
Cys	Ala	Tyr	Val												
			65												

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Val Asp Ala Arg Leu Arg Thr Phe Thr Asp Trp Pro Ile Ser Asn Ile
1 5 10 15
Gln Pro Ala Ser Ala Leu Ala Gln Ala Gly Leu Tyr Tyr Gln Lys Ile
20 25 30
Gly Asp Gln Val Arg Cys Phe His Cys Asn Ile Gly Leu Arg Ser Trp
35 40 45
Gln Lys Glu Asp Glu Pro Trp Phe Glu His Ala Lys Trp Ser Pro Lys
50 55 60
Cys Gln Phe Val
65

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Ser Val Arg Leu Ala Thr Phe Gly Glu Trp Pro Leu Asn Ala Pro
1 5 10 15
Val Ser Ala Glu Asp Leu Val Ala Asn Gly Phe Phe Gly Thr Trp Met
20 25 30
Glu Ala Glu Cys Asp Phe Cys His Val Arg Ile Asp Arg Trp Glu Tyr
35 40 45
Gly Asp Leu Val Ala Glu Arg His Arg Arg Ser Ser Pro Ile Cys Ser
50 55 60
Met Val
65

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

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Glu Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met
 1 5 10 15
 Asp Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val
 20 25 30
 Cys Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
 35 40 45

(i) **SEQUENCE CHARACTERISTICS:**

- (A) **LENGTH:** 46 amino acids
- (B) **TYPE:** amino acid
- (C) **STRANDEDNESS:** not relevant
- (D) **TOPOLOGY:** both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu Gln Leu Arg Arg Leu Pro Glu Glu Arg Thr Cys Lys Val Cys Met
1 5 10 15

Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val
20 25 30

Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
35 40 45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Ser Lys Ile Cys Met
 1 5 10 15
 Asp Arg Asn Ile Ala Ile Val Phe Phe Pro Cys Gly His Leu Ala Thr
 20 25 30
 Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
(B) ~~TYPE: amino acid~~
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Cys Lys Ile Cys Met
1 5 10 15

Asp Arg Asn Ile Ala Ile Val Phe Val Pro Cys Gly His Leu Val Thr
20 25 30

Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
35 40 45

(2) INFORMATION FOR SEO ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Glu Asn Arg Gln Leu Lys Asp Ala Arg Leu Cys Lys Val Cys Leu
1 5 10 15

Asp Glu Glu Val Gly Val Val Phe Leu Pro Cys Gly His Leu Ala Thr
20 25 30

Cys Asn Gln Cys Ala Pro Ser Val Ala Asn Cys Pro Met Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Lys Glu Pro Gln Val Glu Asp Ser Lys Leu Cys Lys Ile Cys Tyr
1 5 10 15
Val Glu Glu Cys Ile Val Cys Phe Val Pro Cys Gly His Val Val Ala
20 25 30
Cys Ala Lys Cys Ala Leu Ser Val Asp Lys Cys Pro Met Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala Val Glu Ala Glu Val Ala Asp Asp Arg Leu Cys Lys Ile Cys Leu
1 5 10 15
Gly Ala Glu Lys Thr Val Cys Phe Val Pro Cys Gly His Val Val Ala
20 25 30
Cys Gly Lys Cys Ala Ala Gly Val Thr Thr Cys Pro Val Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAATTCCGGG AGACCTACAC CCCCGGAGAT CAGAGGTCAT TGCTGGCGTT CAGAGCCTAG 60
GAAGTGGGCT GCGGTATCAG CCTAGCAGTA AAACCGACCA GAAGCCATGC ACAAAACTAC 120
ATCCCCAGAG AAAGACTTGT CCCTTCCCCT CCCTGTCATC TCACCATGAA CATGGTTCAA 180
GACAGCGCCT TTCTAGCCAA GCTGATGAAG AGTGCTGACA CCTTTGAGTT GAAGTATGAC 240
TTTCCTGTG AGCTGTACCG ATTGTCCACG TATTCAGCTT TCCCAGGGG AGTTCCTGTG 300
TCAGAAAGGA GTCTGGCTCG TGCTGGCTTT TACTACACTG GTGCCAATGA CAAGGTCAAG 360

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TGCTTCTGCT	GTGGCCTGAT	GCTAGACAAC	TGGAAACAAG	GGGACAGTCC	CATGGAGAAG	420
CACAGAAAGT	TGTACCCCAG	CTGCAACTTT	GTACAGACTT	TGAATCCAGC	CAACAGTCTG	480
GAAGCTAGTC	CTCGGCCTTC	TCTTCCTTCC	ACGGCGATGA	GCACCATGCC	TTTGAGCTTT	540
GCAAGTTCTG	AGAATACTGG	CTATTTTCAGT	GGCTCTTACT	CGAGCTTTCC	CTCAGACCCT	600
GTGAACTTCC	GAGCAAATCA	AGATTGTCCT	GCTTTGAGCA	CAAGTCCCTA	CCACTTTGCA	660
ATGAACACAG	AGAAGGCCAG	ATTACTCACC	TATGAAACAT	GGCCATTGTC	TTTTCTGTCA	720
CCAGCAAAGC	TGGCCAAAGC	AGGCTTCTAC	TACATAGGAC	CTGGAGATAG	AGTGGCCTGC	780
TTTGCGTGCG	ATGGGAAACT	GAGCAACTGG	GAACGTAAAG	ATGATGCTAT	GTCAGAGCAC	840
CAGAGGCATT	TCCCCAGCTG	TCCGTTCTTA	AAAGACTTGG	GTCAGTCTGC	TTCGAGATAC	900
ACTGTCTCTA	ACCTGAGCAT	GCAGACACAC	GCAGCCCGTA	TTAGAACATT	CTCTAACTGG	960
CCTTCTAGTG	CACTAGTTCA	TTCCAGGAA	CTTGCAAGTG	CGGGCTTTTA	TTATACAGGA	1020
CACAGTGATG	ATGTCAAGTG	TTTATGCTGT	GATGGTGGGC	TGAGGTGCTG	GGAATCTGGA	1080
GATGACCCCT	GGGTGGAACA	TGCCAAGTGG	TTTCCAAGGT	GTGAGTACTT	GCTCAGAATC	1140
AAAGGCCAAG	AATTTGTCAG	CCAAGTTCAA	GCTGGCTATC	CTCATCTACT	TGAGCAGCTA	1200
TTATCTACGT	CAGACTCCCC	AGAAGATGAG	AATGCAGACG	CAGCAATCGT	GCATTTTGGC	1260
CCTGGAGAAA	GTTCGGAAGA	TGTCGTCATG	ATGAGCACGC	CTGTGGTTAA	AGCAGCCTTG	1320
GAAATGGGCT	TCAGTAGGAG	CCTGGTGAGA	CAGACGGTTC	AGTGGCAGAT	CCTGGCCACT	1380
GGTGAGAACT	ACAGGACCGT	CAGTGACCTC	GTTATAGGCT	TACTCGATGC	AGAAGACGAG	1440
ATGAGAGAGG	AGCAGATGGA	GCAGGCGGCC	GAGGAGGAGG	AGTCAGATGA	TCTAGCACTA	1500
ATCCGGAAGA	ACAAAATGGT	GCTTTTCCAA	CATTTGACGT	GTGTGACACC	AATGCTGTAT	1560
TGCCTCCTAA	GTGCAAGGGC	CATCACTGAA	CAGGAGTGCA	ATGCTGTGAA	ACAGAAACCA	1620
CACACCTTAC	AAGCAAGCAC	ACTGATTGAT	ACTGTGTTAG	CAAAAGGAAA	CACTGCAGCA	1680
ACCTCATTCA	GAAACTCCCT	TCGGGAAATT	GACCCTGCGT	TATACAGAGA	TATATTTGTG	1740
CAACAGGACA	TTAGGAGTCT	TCCCACAGAT	GACATTGCAG	CTCTACCAAT	GGAAGAACAG	1800
TTGCGGCCCC	TCCCGGAGGA	CAGAATGTGT	AAAGTGTGTA	TGGACCGAGA	GGTATCCATC	1860
GTGTTCATTC	CCTGTGGCCA	TCTGGTCGTG	TGCAAAGACT	GCGCTCCCTC	TCTGAGGAAG	1920
TGTCCCATCT	GTAGAGGGAC	CATCAAGGGC	ACAGTGCGCA	CATTTCTCTC	CTGAACAAGA	1980
CTAATGGTCC	ATGGCTGCAA	CTTCAGCCAG	GAGGAAGTTC	ACTGTCACTC	CCAGTTCCAT	2040
TCGGAACCTG	AGGCCAGCCT	GGATAGCACG	AGACACCGCC	AAACACACAA	ATATAAACAT	2100
GAAAAACTTT	TGTCTGAAGT	CAAGAATGAA	TGAATTACTT	ATATAATAAT	TTAATTGGT	2160
TTCTTAAAA	GTGCTATTTG	TTCCCAACTC	AGAAAATTGT	TTTCTGTAAA	CATATTTACA	2220

TACTACCTGC ATCTAAAGTA TTCATATATT CATATATTCA GATGTCATGA GAGAGGGTTT	2280
TGTTCTTGTT CCTGAAAAGC TGGTTTATCA TCTGATCAGC ATATACTGCG CAACGGGCAG	2340
GGCTAGAATC CATGAACCAA GCTGCAAAGA TCTCACGCTA AATAAGGCGG AAAGATTG	2400
AGAAACGAAA GGAAATTCTT TCCTGTCCAA TGTATACTCT TCAGACTAAT GACCTCTTCC	2460
TATCAAGCCT TCTA	2474

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met 1	Asn	Met	Val	Gln 5	Asp	Ser	Ala	Phe	Leu 10	Ala	Lys	Leu	Met	Lys 15	Ser
Ala	Asp	Thr	Phe 20	Glu	Leu	Lys	Tyr	Asp 25	Phe	Ser	Cys	Glu	Leu 30	Tyr	Arg
Leu	Ser	Thr 35	Tyr	Ser	Ala	Phe	Pro 40	Arg	Gly	Val	Pro	Val 45	Ser	Glu	Arg
Ser	Leu 50	Ala	Arg	Ala	Gly	Phe 55	Tyr	Tyr	Thr	Gly	Ala 60	Asn	Asp	Lys	Val
Lys 65	Cys	Phe	Cys	Cys	Gly 70	Leu	Met	Leu	Asp	Asn 75	Trp	Lys	Gln	Gly	Asp 80
Ser	Pro	Met	Glu	Lys 85	His	Arg	Lys	Leu	Tyr 90	Pro	Ser	Cys	Asn	Phe 95	Val
Gln	Thr	Leu	Asn 100	Pro	Ala	Asn	Ser	Leu 105	Glu	Ala	Ser	Pro	Arg 110	Pro	Ser
Leu	Pro	Ser 115	Thr	Ala	Met	Ser	Thr 120	Met	Pro	Leu	Ser	Phe 125	Ala	Ser	Ser
Glu	Asn 130	Thr	Gly	Tyr	Phe	Ser 135	Gly	Ser	Tyr	Ser	Ser 140	Phe	Pro	Ser	Asp
Pro 145	Val	Asn	Phe	Arg	Ala 150	Asn	Gln	Asp	Cys	Pro 155	Ala	Leu	Ser	Thr	Ser 160
Pro	Tyr	His	Phe	Ala 165	Met	Asn	Thr	Glu	Lys 170	Ala	Arg	Leu	Leu	Thr 175	Tyr
Glu	Thr	Trp	Pro 180	Leu	Ser	Phe	Leu	Ser 185	Pro	Ala	Lys	Leu	Ala 190	Lys	Ala
Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys

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195					200					205					
Asp	Gly	Lys	Leu	Ser	Asn	Trp	Glu	Arg	Lys	Asp	Asp	Ala	Met	Ser	Glu
210						215					220				
His	Gln	Arg	His	Phe	Pro	Ser	Cys	Pro	Phe	Leu	Lys	Asp	Leu	Gly	Gln
225					230					235					240
Ser	Ala	Ser	Arg	Tyr	Thr	Val	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala
				245					250					255	
Ala	Arg	Ile	Arg	Thr	Phe	Ser	Asn	Trp	Pro	Ser	Ser	Ala	Leu	Val	His
			260					265					270		
Ser	Gln	Glu	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	His	Ser	Asp
		275					280					285			
Asp	Val	Lys	Cys	Leu	Cys	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser
	290					295					300				
Gly	Asp	Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu
305					310					315					320
Tyr	Leu	Leu	Arg	Ile	Lys	Gly	Gln	Glu	Phe	Val	Ser	Gln	Val	Gln	Ala
				325					330					335	
Gly	Tyr	Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Ser	Pro
			340					345					350		
Glu	Asp	Glu	Asn	Ala	Asp	Ala	Ala	Ile	Val	His	Phe	Gly	Pro	Gly	Glu
		355					360					365			
Ser	Ser	Glu	Asp	Val	Val	Met	Met	Ser	Thr	Pro	Val	Val	Lys	Ala	Ala
		370				375					380				
Leu	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Arg	Gln	Thr	Val	Gln	Trp
385					390					395					400
Gln	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Thr	Val	Ser	Asp	Leu	Val
				405					410					415	
Ile	Gly	Leu	Leu	Asp	Ala	Glu	Asp	Glu	Met	Arg	Glu	Glu	Gln	Met	Glu
			420				425						430		
Gln	Ala	Ala	Glu	Glu	Glu	Glu	Ser	Asp	Asp	Leu	Ala	Leu	Ile	Arg	Lys
		435					440					445			
Asn	Lys	Met	Val	Leu	Phe	Gln	His	Leu	Thr	Cys	Val	Thr	Pro	Met	Leu
		450				455					460				
Tyr	Cys	Leu	Leu	Ser	Ala	Arg	Ala	Ile	Thr	Glu	Gln	Glu	Cys	Asn	Ala
465					470					475					480
Val	Lys	Gln	Lys	Pro	His	Thr	Leu	Gln	Ala	Ser	Thr	Leu	Ile	Asp	Thr
				485					490					495	
Val	Leu	Ala	Lys	Gly	Asn	Thr	Ala	Ala	Thr	Ser	Phe	Arg	Asn	Ser	Leu
			500					505					510		
Arg	Glu	Ile	Asp	Pro	Ala	Leu	Tyr	Arg	Asp	Ile	Phe	Val	Gln	Gln	Asp
		515					520					525			

Ile Arg Ser Leu Pro Thr Asp Asp Ile Ala Ala Leu Pro Met Glu Glu
530 535 540

Gln Leu Arg Pro Leu Pro Glu Asp Arg Met Cys Lys Val Cys Met Asp
545 550 555 560

Arg Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val Cys
565 570 575

Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg Gly Thr
580 585 590

Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
595 600

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGTGGTGGG	GATCTATTGT	CCAAGTGGTG	AGAAACTTCA	TCTGGAAGTT	TAAGCGGTCA	60
GAAATACTAT	TACTACTCAT	GGACAAAACT	GTCTCCAGA	GA CTGCCCCA	AGGTACCTTA	120
CACCCAAAAA	CTTAAACGTA	TAATGGAGAA	GAGCACAATC	TTGTCAAATT	GGACAAAGGA	180
GAGCGAAGAA	AAAATGAAGT	TTGACTTTTC	GTGTGAACTC	TACCGAATGT	CTACATATTC	240
AGCTTTTCCC	AGGGGAGTTC	CTGTCTCAGA	GAGGAGTCTG	GCTCGTGCTG	GCTTTTATTA	300
TACAGGTGTG	AATGACAAAG	TCAAGTGCTT	CTGCTGTGGC	CTGATGTTGG	ATAACTGGAA	360
ACAAGGGGAC	AGTCCTGTTG	AAAAGCACAG	ACAGTTCTAT	CCCAGCTGCA	GCTTTGTACA	420
GA CTCTGCTT	TCAGCCAGTC	TGCAGTCTCC	ATCTAAGAAT	ATGTCTCCTG	TGAAAAGTAG	480
ATTTGCACAT	TCGTACCTC	TGGAACGAGG	TGGCATTAC	TCCAACCTGT	GCTCTAGCCC	540
TCTTAATTCT	AGAGCAGTGG	AAGACTTCTC	ATCAAGGATG	GATCCCTGCA	GCTATGCCAT	600
GAGTACAGAA	GAGGCCAGAT	TTCTTACTTA	CAGTATGTGG	CCTTTAAGTT	TTCTGTCAAC	660
AGCAGAGCTG	GCCAGAGCTG	GCTTCTATTA	CATAGGGCCT	GGAGACAGGG	TGGCCTGTTT	720
TGCCTGTGGT	GGGAAACTGA	GCAACTGGGA	ACCAAAGGAT	TATGCTATGT	CAGAGCACCG	780
CAGACATTTT	CCCCACTGTC	CATTTCTGGA	AAATACTTCA	GAAACACAGA	GGTTTAGTAT	840
ATCAAATCTA	AGTATGCAGA	CACACTCTGC	TCGATTGAGG	ACATTTCTGT	ACTGGCCACC	900
TAGTGTTCCT	GTTCAGCCCCG	AGCAGCTTGC	AAGTGCTGGA	TTCTATTACG	TGGATCGCAA	960

TGATGATGTC AAGTGCCTTT GTTGTGATGG TGGCTTGAGA TGTGGGAAC CTGGAGATGA	1020
CCCCTGGATA GAACACGCCA AATGGTTTCC AAGGTGTGAG TTCTTGATAC GGATGAAGGG	1080
TCAGGAGTTT GTTGATGAGA TTCAAGCTAG ATATCCTCAT CTTCTTGAGC AGCTGTTGTC	1140
CACTTCAGAC-ACCCAGGAG-AAGAAAATGC-TGACCTACA-GAGACAGTGG-TGCATTTTGG	1200
CCCTGGAGAA AGTTCGAAAG ATGTCGTCAT GATGAGCAGC CCTGTGGTTA AAGCAGCCTT	1260
GGAAATGGGC TTCAGTAGGA GCCTGGTGAG ACAGACGGTT CAGCGGCAGA TCCTGGCCAC	1320
TGGTGAGAAC TACAGGACCG TCAATGATAT TGTCTCAGTA CTTTGAATG CTGAAGATGA	1380
GAGAAGAGAA GAGGAGAAGG AAAGACAGAC TGAAGAGATG GCATCAGGTG ACTTATCACT	1440
GATTCCGAAG AATAGAATGG CCCTCTTTCA ACAGTTGACA CATGTCCTTC CTATCCTGGA	1500
TAATCTTCTT GAGGCCAGTG TAATTACAAA ACAGGAACAT GATATTATTA GACAGAAAAC	1560
ACAGATACCC TTACAAGCAA GAGAGCTTAT TGACACCGTT TTAGTCAAGG GAAATGCTGC	1620
AGCCAACATC TTCAAAAACCT CTCTGAAGGG AATTGACTCC ACGTTATATG AAAACTTATT	1680
TGTGGAAAAG AATATGAAGT ATATTCCAAC AGAAGACGTT TCAGGCTTGT CATTGGAAGA	1740
GCAGTTGCGG AGATTACAAG AAGAACGAAC TTGCAAAGTG TGTATGGACA GAGAGGTTTC	1800
TATTGTGTTT ATTCCGTGTG GTCATCTAGT AGTCTGCCAG GAATGTGCCC CTTCTCTAAG	1860
GAAGTGCCCC ATCTGCAGGG GGACAATCAA GGGGACTGTG CGCACATTTT TCTCATGAGT	1920
GAAGAATGGT CTGAAAGTAT TGTGGACAT CAGAAGCTGT CAGAACAAAG AATGAACTAC	1980
TGATTTCAAGC TCTTCAGCAG GACATTCTAC TCTCTTTCAA GATTAGTAAT CTTGCTTTAT	2040
GAAGGGTAGC ATTGTATATT TAAGCTTAGT CTGTTGCAAG GGAAGGTCTA TGCTGTTGAG	2100
CTACAGGACT GTGTCTGTTT CAGAGCAGGA GTTGGGATGC TTGCTGTATG TCCTTCAGGA	2160
CTTCTTGGA TTTGGGAATT TGGGGAAAGC TTTGGAATCC AGTGATGTGG AGCTCAGAAA	2220
TCCTGGAACC AGTGACTCTG GTACTCAGTA GATAGGGTAC CCTGTACTTC TTGGTGCTTT	2280
TCCAGTCTGG GAAATAAGGA GGAATCTGCT GCTGGTAAAA ATTTGCTGGA TGTGAGAAAT	2340
AGATGAAAGT GTTTCGGGTG GGGGCGTGCA TCAGTGTAGT GTGTGCAGGG ATGTATGCAG	2400
GCCAAACACT GTGTAG	2416

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1. **Содержание:** 1. Введение. 2. Описание объекта исследования. 3. Методология исследования. 4. Результаты исследования. 5. Заключение.

87

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Gln	Ala	Arg	Tyr	Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	
				325					330						335	
Thr	Pro	Gly	Glu	Glu	Asn	Ala	Asp	Pro	Thr	Glu	Thr	Val	Val	His	Phe	
			340					345					350			
Gly	Pro	Gly	Glu	Ser	Ser	Lys	Asp	Val	Val	Met	Met	Ser	Thr	Pro	Val	
		355					360					365				
Val	Lys	Ala	Ala	Leu	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Arg	Gln	
	370					375					380					
Thr	Val	Gln	Arg	Gln	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Thr	Val	
385					390					395					400	
Asn	Asp	Ile	Val	Ser	Val	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Arg	Arg	Glu	
			405						410					415		
Glu	Glu	Lys	Glu	Arg	Gln	Thr	Glu	Glu	Met	Ala	Ser	Gly	Asp	Leu	Ser	
			420					425					430			
Leu	Ile	Arg	Lys	Asn	Arg	Met	Ala	Leu	Phe	Gln	Gln	Leu	Thr	His	Val	
	435						440					445				
Leu	Pro	Ile	Leu	Asp	Asn	Leu	Leu	Glu	Ala	Ser	Val	Ile	Thr	Lys	Gln	
	450					455					460					
Glu	His	Asp	Ile	Ile	Arg	Gln	Lys	Thr	Gln	Ile	Pro	Leu	Gln	Ala	Arg	
465					470					475					480	
Glu	Leu	Ile	Asp	Thr	Val	Leu	Val	Lys	Gly	Asn	Ala	Ala	Ala	Asn	Ile	
			485						490					495		
Phe	Lys	Asn	Ser	Leu	Lys	Gly	Ile	Asp	Ser	Thr	Leu	Tyr	Glu	Asn	Leu	
			500					505					510			
Phe	Val	Glu	Lys	Asn	Met	Lys	Tyr	Ile	Pro	Thr	Glu	Asp	Val	Ser	Gly	
		515					520					525				
Leu	Ser	Leu	Glu	Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	
	530					535					540					
Lys	Val	Cys	Met	Asp	Arg	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly	
545					550					555					560	
His	Leu	Val	Val	Cys	Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	
				565					570					575		
Ile	Cys	Arg	Gly	Thr	Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser		
			580					585					590			